

**From:** Hamud, Fozia  
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Fozia Hamud  
Patent Examiner  
Art Unit 1647  
Crystal-Mall-One, Room 10Bo5  
Mail Box CM1-10B19  
308-8891

Point of Contact:  
Toby Port  
Technical Info. Specialist  
CM1 6A04  
703-308-3534

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Searcher: \_\_\_\_\_  
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Searcher Prep/Review: 12  
Clerical: \_\_\_\_\_  
Online time: 12

TYPE OF SEARCH:  
NA Sequences: 1  
AA Sequences: 1  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: g  
WWW/Internet: g  
Other (specify): \_\_\_\_\_



XX WPI: 2002-217048/27.  
DR P-PSDB: AB807626.  
XX New cytokine receptor polypeptide designated zcytor18, useful for  
PT inhibiting cell proliferation associated with psoriasis or tumor  
PT growth, and modulating immune system by binding to endogenous zcytor18  
PT ligand  
XX  
PS Claim 5; Page 85-90; 119pp; English.  
XX  
CC The invention relates to an isolated cytokine receptor polypeptide  
CC designated zcytor18. The zcytor18 polypeptides can be expressed by  
CC standard recombinant methodology. The polypeptides can be used to inhibit  
CC cell proliferation associated with psoriasis or tumor growth. The  
CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in  
CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
CC and localize zcytor18 gene expression in tissue samples. The probes are  
CC also useful for detecting gross aberrations in chromosome 3 in which  
CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
CC linkage-based testing of pulmonary alveolar proteinosis, familial  
CC periodic fever and erythroleukemia, and erythroleukemia associated with  
CC polymorphisms of cytokine receptors. The present sequence represents a  
CC human zcytor18 nucleotide sequence.  
XX  
SQ Sequence 2383 BP; 558 A; 679 C; 538 G; 508 T; 0 other;

Query Match. 100.0%; Score 2383; DB 24; Length 2383;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGCGCGGCGCACCGCCACTCGGGCTGGCCAGCGCGCGCGCGCGCGCGAGAAC 60  
DB 1 CCGCGCGGCGCACCGCCACTCGGGCTGGCCAGCGCGCGCGCGCGCGAGAAC 60  
OY 61 GGCGTGGTGGGGAGCGCAGCGCGATGGCGCGTGGCTGGAGCTCTGCTCCGCTCTTT 120  
DB 61 GGCGTGGTGGGGAGCGCAGCGCGATGGCGCGTGGCTGGAGCTCTGCTCCGCTCTTT 120  
OY 121 TAGCGTCAACGGCTGCCTCAACGGCTGCAGCTGGCTGGCGCGTGGCGGGTCCGCGCG 180  
DB 121 TAGCGTCAACGGCTGCCTCAACGGCTGCAGCTGGCTGGCGCGTGGCGGGTCCGCGCG 180  
OY 181 CGCGCGGCGCGCGCACCTGTGGCTGGAGGATGAAGCGGCTGCCGACCCCGGCTTG 240  
DB 181 CGCGCGGCGCGCGCACCTGTGGCTGGAGGATGAAGCGGCTGCCGACCCCGGCTTG 240  
OY 241 TGTGCTAATAGGAGTGGGGCCAGCCAGCAGAACAGTGGGCTGTACAAATCAACCTT 300  
DB 241 TGTGCTAATAGGAGTGGGGCCAGCCAGCAGAACAGTGGGCTGTACAAATCAACCTT 300  
OY 301 CAATATGACAAATGTACCACTTGAATCCAGTGGGAGAGCATGTGATGCTGACG 360  
DB 301 CAATATGACAAATGTACCACTTGAATCCAGTGGGAGAGCATGTGATGCTGACG 360  
OY 361 CCAGAAATACCAATCAGCCAGTATGCTGCCATGACCAAGTGGCAGTCAACCTTTTG 420  
DB 361 CCAGAAATACCAATCAGCCAGTATGCTGCCATGACCAAGTGGCAGTCAACCTTTTG 420  
OY 421 GTCCCGAGGGCGCTCGGCATGAAATCTTGAAGGATTTGGGTAATCTGGAGAGCT 480  
DB 421 GTCCCGAGGGCGCTCGGCATGAAATCTTGAAGGATTTGGGTAATCTGGAGAGCT 480  
OY 481 GAAGTCGGAGGAGACAGTGCACCAACTGATTTAAAGGATCCGAGAGCTCAACAG 540  
DB 481 GAAGTCGGAGGAGACAGTGCACCAACTGATTTAAAGGATCCGAGAGCTCAACAG 540  
OY 541 TAGCTCAAAAGACTGGAATGGAATCTCAACCTTTCTGATATGAATTTGAACGGA 600  
DB 541 TAGCTCAAAAGACTGGAATGGAATCTCAACCTTTCTGATATGAATTTGAACGGA 600  
OY 601 TTATTCGTAAAGTTGTCCCTTTTCTTCATTAACAAAGCAATTAACACCTTT 660

DB 601 TTATTCGTAAAGTTGTCCCTTTTCTTCATTAACAAAGCAATTAACACCTTT 660  
OY 661 CTTCTTTAGAACCGCGCTGTGACCTGTGTTTACAGCGGAGCAATCTAGCTTGTAAAC 720  
DB 661 CTTCTTTAGAACCGCGCTGTGACCTGTGTTTACAGCGGAGCAATCTAGCTTGTAAAC 720  
OY 721 CTTCTGGAAGCTCGGAACCTGAAACATCAGCCAGCATGCTCGGACATGCTGCTT 780  
DB 721 CTTCTGGAAGCTCGGAACCTGAAACATCAGCCAGCATGCTCGGACATGCTGCTT 780  
OY 781 CGAACCATGACCGGACCACTTTCGCTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTT 840  
DB 781 CGAACCATGACCGGACCACTTTCGCTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTT 840  
OY 841 CGAAGGACCTTTCAAGCGGAAGACCTGTGAAGGAGGCAAACTACAGAGACGACCTG 900  
DB 841 CGAAGGACCTTTCAAGCGGAAGACCTGTGAAGGAGGCAAACTACAGAGACGACCTG 900  
OY 901 CCTCTCTCAAAATGTTTCTCCAGGGGATTAATAATTTAGCTGGTGGATGACATACAC 960  
DB 901 CCTCTCTCAAAATGTTTCTCCAGGGGATTAATAATTTAGCTGGTGGATGACATACAC 960  
OY 961 AACAGAAAGCTGATGATTAATGCTTAAAGCCAGTGCACCTCCCGTGGCGGGGCCAT 1020  
DB 961 AACAGAAAGCTGATGATTAATGCTTAAAGCCAGTGCACCTCCCGTGGCGGGGCCAT 1020  
OY 1021 CAGAGCGGTGGCCATFACAGTGGCACTGTGTAGTCAATATCGGCAATTCGGAGCTTTCAC 1080  
DB 1021 CAGAGCGGTGGCCATFACAGTGGCACTGTGTAGTCAATATCGGCAATTCGGAGCTTTCAC 1080  
OY 1081 TGTGATGTGGCGCAAGGAAACCAAGAAATATATATTCACATTTAGATGAAGAGCTC 1140  
DB 1081 TGTGATGTGGCGCAAGGAAACCAAGAAATATATATTCACATTTAGATGAAGAGCTC 1140  
OY 1141 TGAGTCTTCCACATACACTGCAGCTCCAGAGAGAGCTCCGCGCGCGCGCGAGGT 1200  
DB 1141 TGAGTCTTCCACATACACTGCAGCTCCAGAGAGAGCTCCGCGCGCGCGCGAGGT 1200  
OY 1201 CTTTCTCTCTATTTCCAGTAAAGTGGCCAGATCAGATGAATGTCTCCAGTGTTCG 1260  
DB 1201 CTTTCTCTCTATTTCCAGTAAAGTGGCCAGATCAGATGAATGTCTCCAGTGTTCG 1260  
OY 1261 CTACTTCTCCAGACTTCTGTGGCTGTGAGTGGCTGTGGACCTGTGGAGAGCTTCAG 1320  
DB 1261 CTACTTCTCCAGACTTCTGTGGCTGTGAGTGGCTGTGGAGAGCTTCAG 1320  
OY 1321 CCTCTGTAGAGAGGCGAGAGCAATGGGTTCATCCAGAGATCCACAGAGTCCAGATTCAT 1380  
DB 1321 CCTCTGTAGAGAGGCGAGAGCAATGGGTTCATCCAGAGATCCACAGAGTCCAGATTCAT 1380  
OY 1381 CATCTGCTTGTTCCTCAAGCTATGAGTACTTGTGGACAGAGAGACTACAAACAA 1440  
DB 1381 CATCTGCTTGTTCCTCAAGCTATGAGTACTTGTGGACAGAGAGACTACAAACAA 1440  
OY 1441 AGAGTGGCGCGAGCTCGGGGAAAGAGAGCTCTTCTCTGGTGGCGGTGTACGCTTTC 1500  
DB 1441 AGAGTGGCGCGAGCTCGGGGAAAGAGAGCTCTTCTCTGGTGGCGGTGTACGCTTTC 1500  
OY 1501 CGAAGACTCCGCGAGCGCAGAGAGTGTCTCCGCGGCTCAGCAAGTTTATCCGCT 1560  
DB 1501 CGAAGACTCCGCGAGCGCAGAGAGTGTCTCCGCGGCTCAGCAAGTTTATCCGCT 1560  
OY 1561 CTACTTTGATTTCTCTCGAGGAGAGCTCCCGGTATCTCTAGACCTGAGTACCAAGTA 1620  
DB 1561 CTACTTTGATTTCTCTCGAGGAGAGCTCCCGGTATCTCTAGACCTGAGTACCAAGTA 1620  
OY 1621 CAGACTCATGACAACTTCTCTCAGCTGTTCCTCACTTGCACCTCCGAGACAGCGCT 1680  
DB 1621 CAGACTCATGACAACTTCTCTCAGCTGTTCCTCACTTGCACCTCCGAGACAGCGCT 1680  
OY 1681 CCAGAGCGCGGCGCAGCAGCGAGCGGAGAGAACTACTTCCGAGAGCAAGTC 1740











Db 329 CTTGCCATGACCAAGTGGCAGTCCACATTTCTTTGGTCCCGAGGGCCCTCGGCATCGAAT 388  
QY 447 TCTTGAAGAGATTTCCGGGTAAATCTGGAGAGCTGAAGTCCGAGGGGAAGACAGTGCAC 506  
Db 389 TCTTGAAGAGATTTCCGGGTAAATCTGGAGAGCTGAAGTCCGAGGGGAAGACAGTGCAC 448  
QY 507 AACTCATTTAAAGATCCGAAGCAGCTCAACAGTAGCTTCMAAAGACTGGATGGAAT 566  
Db 449 AACTCATTTAAAGATCCGAAGCAGCTCAACAGTAGCTTCMAAAGACTGGATGGAAT 508  
QY 567 CTCACCTTTCTCTGAATATGAAATTTGAAACGGATTATTTCTGTAAGGTTGTCCTTTTC 626  
Db 509 CTCACCTTTCTCTGAATATGAAATTTGAAACGGATTATTTCTGTAAGGTTGTCCTTTTC 626  
QY 627 CTTCCATTAAGAAAGCAATTAACACCTTTCTCTGTAAGCCTCGAGCTGTGACC 686  
Db 566 CTTCCATTAAGAAAGCAATTAACACCTTTCTCTGTAAGCCTCGAGCTGTGACC 625  
QY 687 TCTTGTACAGCGGCAATCTAGCTTTGAAACCTTTCTGGAAGCTTCGGAAGCTTCGGAACA 746  
Db 626 TCTTGTACAGCGGCAATCTAGCTTTGAAACCTTTCTGGAAGCTTCGGAAGCTTCGGAACA 685  
QY 747 TCAGCAGCAGTGGCTCGGACATCGAGTGTCTTCGACCATGACCGCAACCTTCGGCT 806  
Db 686 TCAGCAGCAGTGGCTCGGACATCGAGTGTCTTCGACCATGACCGCAACCTTCGGCT 745  
QY 807 TCGTGTCTTCTATCTTCACTACAGCTTCAGCAGGAGGACCTTCGAGGCAAGACCT 866  
Db 746 TCGTGTCTTCTATCTTCACTACAGCTTCAGCAGGAGGACCTTCGAGGCAAGACCT 805  
QY 867 GTAAGCAGGAGCAAACTACAGAGACACGAGCTGCTCTTCAAAATGTTTCTCCAGGG 926  
Db 806 GTAAGCAGGAGCAAACTACAGAGATGACGAGCTGCTCTTCAAAATGTTTCTCCAGGG 865  
QY 927 ATTATATATTTAGCTGGTGGATGACATCTACACACAGAAAGTGTATGCTATGCT 986  
Db 866 ATTATATATTTAGCTGGTGGATGACATCTACACACAGAAAGTGTATGCTATGCT 925  
QY 987 TAAAGCCAGTGCATCCCGTGGCGGGCCCATCAGAGCGGTGGCCATCAGAGTGCAC 1046  
Db 926 TAAAGCCAGTGCATCCCGTGGCGGGCCCATCAGAGCGGTGGCCATCAGAGTGCAC 985  
QY 1047 TGGTAGTCATATGGATTCGCGAGCTCTTCACTGTGATGTGCGCAGAGACCAAG 1106  
Db 986 TGGTAGTCATATGGATTCGCGAGCTCTTCACTGTGATGTGCGCAGAGACCAAG 1045  
QY 1107 AAATATATATTCATTTAGATGAAGAGCTCTGAGTCTTCCACATACACTGCAGCAC 1166  
Db 1046 AAATATATATTTACATTTAGATGAAGAGCTCTGAGTCTTCCACATACACTGCAGCAC 1105  
QY 1167 TCCCAAGAGAGAGCTCCGGCCGCGCGGCGGAGGCTTTCTCTGCTATTCAGTAAGATG 1226  
Db 1106 TCCCAAGAGAGAGCTCCGGCCGCGCGGCGGAGGCTTTCTCTGCTATTCAGTAAGATG 1165  
QY 1227 GCCAGATCATGATGTGCTCCAGTGTTCGCTACTTCTCCAGGACTTCTGTGCT 1286  
Db 1166 GCCAGATCATGATGTGCTCCAGTGTTCGCTACTTCTCCAGGACTTCTGTGCT 1225  
QY 1287 GTGAGGTGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGAGAGAGGCGAGAGAT 1346  
Db 1226 GTGAGGTGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGAGAGAGGCGAGAGAT 1285  
QY 1347 GGGTCATCAGAGATCCAGAGTCCAGTTCATCTATGTTGTTTCCAAAGTATGA 1406  
Db 1286 GGGTCATCAGAGATCCAGAGTCCAGTTCATCTATGTTGTTTCCAAAGTATGA 1345  
QY 1407 AGTACTTTGTGGACAAGAAAGTACAAACAAAGAGGTGGCCGAGCTCGGGGAAG 1466  
Db 1346 AGTACTTTGTGGACAAGAAAGTACAAACAAAGAGGTGGCCGAGCTCGGGGAAG 1405  
QY 1467 GAGAGCTTCTCTGGTGGGGTGTGAGCCATTCGCCAAAGAGTCCGCCAGGCCACAGAGA 1526  
Db 1406 GAGAGCTTCTCTGGTGGGGTGTGAGCCATTCGCCAAAGAGTCCGCCAGGCCACAGAGA 1465

QY 1527 GTTCGTCCCGCGGCTCAGCAAGTTTATCGCGGTCTACTTTTGATTATTTCTCGGAGGAG 1586  
Db 1466 GTTCGTCCCGCGGCTCAGCAAGTTTATCGCGGTCTACTTTTGATTATTTCTCGGAGGAG 1525  
QY 1587 AGTCCCGGTATCTCTAGACCTTGAGTACCAAGTACAGACTCATGACATCTTCTCTCAGC 1646  
Db 1526 AGTCCCGGTATCTCTAGACCTTGAGTACCAAGTACAGACTCATGACATCTTCTCTCAGC 1585  
QY 1647 TCTCTTCCCACTTTGCACTCCCGAGACACCGGCTCCAGGAGCGGGCGGAGCACACGCGAC 1706  
Db 1586 TCTCTTCCCACTTTGCACTCCCGAGACACCGGCTCCAGGAGCGGGCGGAGCACACGCGAC 1645  
QY 1707 AGGCGACAGCAAGAACTACTTCCGAGCAAGTCCAGCGGCTCCCTATAGTCGCGCATTT 1766  
Db 1646 AGGCGACAGCAAGAACTACTTCCGAGCAAGTCCAGCGGCTCCCTATAGTCGCGCATTT 1705  
QY 1767 GCAACATGCACCACTTTATTTGAGAGGAGCGGCTGCTGTTTGAAGAGAGTTCGTTCCCT 1826  
Db 1706 GCAACATGCACCACTTTATTTGAGAGGAGCGGCTGCTGTTTGAAGAGAGTTCGTTCCCT 1765  
QY 1827 TCCATCTCTCTCCACTTCCGCTACCGGAGGAGCTTCTTGGAGAAATTTGATTCTGGGCTTGG 1886  
Db 1766 TCCATCTCTCTCCACTTCCGCTACCGGAGGAGCTTCTTGGAGAAATTTGATTCTGGGCTTGG 1825  
QY 1887 TTTTAAATGATGATGTGCAAAACAGGCGCTGAGAGTACTTCTGCTTAAAGGTAGAGG 1946  
Db 1826 TTTTAAATGATGATGTGCAAAACAGGCGCTGAGAGTACTTCTGCTTAAAGGTAGAGG 1885  
QY 1947 CGGCTGTTCTTGGGCAACCGGACCGGCTCCAGCAGCAGAGTCCAGCATGGGGCC 2006  
Db 1886 CGGCTGTTCTTGGGCAACCGGACCGGCTCCAGCAGCAGAGTCCAGCATGGGGCC 1945  
QY 2007 TGGACCAAGAGCGGGAGGCGCGGCTTGGAGGTAGCGGCGCTTGAACCCCTGAC 2066  
Db 1946 TGGACCAAGAGCGGGAGGCGCGGCTTGGAGGTAGCGGCGCTTGAACCCCTGAC 2005  
QY 2067 TGCACACGGTGAAGCGGCGGAGCTCCGAGCATGCGCGGAGCTCAGGCATCTATGACT 2126  
Db 2006 TGCACACGGTGAAGCGGCGGAGCTCCGAGCATGCGCGGAGCTCAGGCATCTATGACT 2065  
QY 2127 CGTCTGTGCGCTCATCCGAGCTGTCTCTGCGACTGTGAGAGGACTCTCGAGGACCA 2186  
Db 2066 CGTCTGTGCGCTCATCCGAGCTGTCTCTGCGACTGTGAGAGGACTCTCGAGGACCA 2125  
QY 2187 CAGAAACGCTTCTCCCTGAGCGGAGCGGTGCTCTCTTCCAGGCTTGGGTGAGGAGAAC 2246  
Db 2126 CAGAAACGCTTCTCCCTGAGCGGAGCGGTGCTCTCTTCCAGGCTTGGGTGAGGAGAAC 2185  
QY 2247 CTCTGTGCGCTTCTCTCCAGCTCTCTCTTCTGCGTCCATCAAGCAGATCTTGGTTGCC 2306  
Db 2186 CTCTGTGCGCTTCTCTCCAGCTCTCTCTTCTGCGTCCATCAAGCAGATCTTGGTTGCC 2245  
QY 2307 GCAGCTACACTGATGAACCTCCAGCGGCTCGCGGCTTGGTAAACAAACGAGAGTCTAAG 2366  
Db 2246 GCAGCTACACTGATGAACCTCCAGCGGCTCGCGGCTTGGTAAACAAACGAGAGTCTAAG 2305  
QY 2367 CATTTGCCACTTTAGCTG 2383  
Db 2306 CATTTGCCACTTTAGCTG 2322

## RESULT 5

AAS15346  
ID AAS15346 standard; cDNA; 3083 BP.

AC AAS15346;

XX  
XX  
XX 13-FEB-2002 (first entry)

DE DNA encoding human Interleukin 17 (hIL-17) receptor like protein.  
XX Interleukin 17; hIL-17 receptor like protein; Immunomodulatory;



Db 1039 TCCTCCATACACTCCAGACATCCCAAGAGAGAGGCTCCGGCGCGGCGGAGGCTTTT 1098  
QY 1205 CTCCTGCTATTCCAGTAAGATGCCAGAAATCACATGAATGCTCCAGTGTTCCTCTAC 1264  
Db 1099 CTCCTGCTATTCCAGTAAGATGCCAGAAATCACATGAATGCTCCAGTGTTCCTCTAC 1158  
QY 1265 TTCCTCAGGACTTCTGTGGCTGTGAGGTGCTCGACCTGTGGGAAGACTTCAGCTC 1324  
Db 1159 TTCCTCAGGACTTCTGTGGCTGTGAGGTGCTCGACCTGTGGGAAGACTTCAGCTC 1218  
QY 1325 TGTAGAGAGGCGAGAGAGATGGGTATCCAGAGATCCACGAGTCCCGAGTTTCATTT 1384  
Db 1219 TGTAGAGAGGCGAGAGAGATGGGTATCCAGAGATCCACGAGTCCCGAGTTTCATTT 1278  
QY 1385 GTGGTTTGTCCAAAGGTATGAATGCTTGTGGCAAGAGAACTTACAAACAAAGGA 1444  
Db 1279 GTGGTTTGTCCAAAGGTATGAATGCTTGTGGCAAGAGAACTTACAAACAAAGGA 1338  
QY 1445 GTGGCGAGGCTCGGGGAAAGAGAGAGCTTCTCTGTGGCGGTGTACGCAATTCGCGAA 1504  
Db 1339 GTGGCGAGGCTCGGGGAAAGAGAGAGCTTCTCTGTGGCGGTGTACGCAATTCGCGAA 1398  
QY 1505 AAGCTCCGCGAGGCGAGAGATGCTGTCGCGGCGCTCAGCAAGTTTATCGCGTCTAC 1564  
Db 1399 AAGCTCCGCGAGGCGAGAGATGCTGTCGCGGCGCTCAGCAAGTTTATCGCGTCTAC 1458  
QY 1565 TTTGATTATTCCTCGAGGAGAGAGCTCCCGGATATCTAGACCTGAGTACCAAGTACAGA 1624  
Db 1459 TTTGATTATTCCTCGAGGAGAGAGCTCCCGGATATCTAGACCTGAGTACCAAGTACAGA 1518  
QY 1625 CTCATGACAAATCTCTCAGCTCTGTCCAGCTTGTCCAGTCCGAGACACGCGCTCCAG 1684  
Db 1519 CTCATGACAAATCTCTCAGCTCTGTCCAGCTTGTCCAGTCCGAGACACGCGCTCCAG 1578  
QY 1685 GAGCGCGGCGAGCACAGCGAGCGGAGAGAACTTCTCGGAGCAAGTCAAGC 1744  
Db 1579 GAGCGCGGCGAGCACAGCGAGCGGAGAGAACTTCTCGGAGCAAGTCAAGC 1638  
QY 1745 CGGTCCCTATACCTCGCCATTTGCAACATGACCAAGTTTATGACGAGGAGCCGAGCTGG 1804  
Db 1639 CGGTCCCTATACCTCGCCATTTGCAACATGACCAAGTTTATGACGAGGAGCCGAGCTGG 1698  
QY 1805 TTCGAAAGAGTGTGTTCCCTTCATCTCTCCTCAGTCCGCTACCGGAGGAGCTGTG 1864  
Db 1699 TTCGAAAGAGTGTGTTCCCTTCATCTCTCCTCAGTCCGCTACCGGAGGAGCTGTG 1758  
QY 1865 GAGAAATTTGATCGGGCTTGTGTTTAAATGATGTCATGTGCAAAACAGGCGCTGAGAT 1924  
Db 1759 GAGAAATTTGATCGGGCTTGTGTTTAAATGATGTCATGTGCAAAACAGGCGCTGAGAT 1818  
QY 1925 GACTTCGCTTAAGTACAGGCGGCTGTTCTGGGGCAACCGAGCAGCGCTCCAG 1984  
Db 1819 GACTTCGCTTAAGTACAGGCGGCTGTTCTGGGGCAACCGAGCAGCGCTCCAG 1878  
QY 1985 CACGAGAGTACAGTGGGGCTGTGGACCAAGAGCGGGAGGCGCGGCTGCGCTGAGCGGT 2044  
Db 1879 CACGAGAGTACAGTGGGGCTGTGGACCAAGAGCGGGAGGCGCGGCTGCGCTGAGCGGT 1938  
QY 2045 AGCGCGGCTTCACCCCTGCTGACACAGCTGAAGCGGCGGAGCGGCTTCGGACATGCGG 2104  
Db 1939 AGCGCGGCTTCACCCCTGCTGACACAGCTGAAGCGGCGGAGCGGCTTCGGACATGCGG 1998  
QY 2105 CGGAGCTACGAGCTATGACTGCTGTGTGCGCTCATCGAGCTGTCTCTGCACTGATG 2164  
Db 1999 CGGAGCTACGAGCTATGACTGCTGTGTGCGCTCATCGAGCTGTCTCTGCACTGATG 2058  
QY 2165 GAGGAGCTTCGAGCGGCGGAGCAAGAGCTTCTCCCTGACGAGAGGCTGTCTCTCT 2224  
Db 2059 GAGGAGCTTCGAGCGGCGGAGCAAGAGCTTCTCCCTGACGAGAGGCTGTCTCTCT 2118  
QY 2225 TCAGGCGTGGTGAGGAGAACTCTCTCGGCTCTCTTCCAAAGCTCTCTCTCTTCTGGGTCA 2284

Db 2119 TCAGGCGTGGTGAGGAGAACTCTCTCGGCTTCTCCAAAGCTCTCTCTCTTCTGGGTCA 2178  
QY 2285 TGCAGAGAGAGTCTGGTTCGGGAGTACACTGATGTAAGTCCAGCGGTGCGCCCTTTG 2344  
Db 2179 TGCAGAGAGAGTCTGGTTCGGGAGTACACTGATGTAAGTCCAGCGGTGCGCCCTTTG 2238  
QY 2345 TAAACAAGCAAGAGTCTTAAGCATTCGCACTTTAGCTG 2383  
Db 2239 TAAACAAGCAAGAGTCTTAAGCATTCGCACTTTAGCTG 2277  
RESULT 6  
ID ABK62082 standard; cDNA; 4392 BP.  
XX AC ABK62082;  
XX DT 18-JUN-2002 (first entry)  
XX DE Human: cDNA encoding novel secreted protein LP253.  
XX KW Human; ss: gene; secreted protein; cancer; autoimmune disease;  
XX KW arthritis; osteoporosis; Alzheimer's disease; Parkinson's disease;  
XX KW meningitis; encephalitis; neoplasia; trauma; ischaemia; infarction;  
XX KW mania; stroke; cardiovascular disease; atherosclerosis; sepsis; anaemia;  
XX KW rheumatoid arthritis; hypothyroidism; allergic response; liver failure;  
XX KW multiple sclerosis; haemorrhage; paraneoplasia; obsessive compulsive disorder;  
XX KW autism; panic disorder; learning disability; feeding disorder;  
XX KW sleep pattern disorder; balance; perception; Th1-dependent insulinitis;  
XX KW adult respiratory distress syndrome; ARDS.  
XX OS Homo sapiens.  
XX PN WO200214358-A2.  
XX PD 21-FEB-2002.  
XX PF 30-JUL-2001; 2001WO-US21124.  
XX PR 11-AUG-2000; 2000US-224642P.  
XX PR 19-OCT-2000; 2000US-241779P.  
XX PA (ELIL) LILLY & CO. ELI.  
XX PI Edmonds BT, Milcanovic R, Ou W, Su EW, Tschang SR, Wang H;  
XX PS P-PSDB; AA091330.  
XX WPI; 2002-304057/34.  
XX PT Novel polypeptides and polynucleotides of secreted proteins useful for  
XX PT treating various diseases such as multiple sclerosis, cancer,  
XX PT autoimmune diseases, osteoporosis, Alzheimer's disease and Parkinson's  
XX PT disease  
PS Claim 1; Page 166-171; 235pp; English.  
XX The invention relates to a novel human secreted polypeptide having  
XX sequence 90% identical to the polypeptide sequences of LP105, LP061,  
XX LP224, LP240, LP239(a), LP243(a), LP243(b), LP253, LP218, LP251(a),  
XX LP252, LP239(b), LP223(a), LP253(a), LP244, LP186, LP251(b), LP255(b),  
XX or LP223(b). Also included are the nucleic acids encoding the LP  
XX proteins (including complement, fragments encoding mature forms of the  
XX polypeptide or variant), a vector comprising the nucleic acid, a  
XX host cell comprising the vector, the preparation of the protein, a  
XX anti-LP antibody, ant/agonists of LP and anti-LP-encoding mRNA  
XX ribozymes. The secreted protein or its agonist is useful in the  
XX manufacture of a medicament for treating a mammal suffering from a  
XX disease (and in diagnosis), condition or disorder associated with  
XX aberrant levels of the secreted protein e.g. cancer, autoimmune diseases,  
XX arthritis, osteoporosis, Alzheimer's disease, Parkinson's disease,  
XX meningitis, encephalitis, neoplasia, trauma, ischaemia and infarction,  
XX mania, stroke, cardiovascular disease, atherosclerosis, rheumatoid  
XX arthritis, hypothyroidism, anaemia, sepsis, allergic responses, multiple

CC sclerosis, liver failure, haemorrhages, paranoia, obsessive compulsive  
 CC disorder, autism, panic disorder, learning disabilities, ALS  
 CC (amyotrophic lateral sclerosis) psychoses, disorders in feeding,  
 CC sleep patterns, balance, and perception, Th1-dependent insulinitis, adult  
 CC respiratory distress syndrome (ARDS). The secreted protein is further  
 CC useful for identifying compounds that bind to the secreted protein. The  
 CC present sequence encodes a novel secreted protein of the invention.  
 XX Sequence 4392 BP; 1125 A; 1050 C; 1101 G; 1116 T; 0 other;

Query Match 90.6%; Score 2158.4; DB 24; Length 4392;  
 Best Local Similarity 98.0%; Pred. No. 0;  
 Matches 2255; Conservative 1; Mismatches 1; Indels 46; Gaps 5;

QY 86 ATGGCCCGTGGCTGACGCTCTGCTCGCTCTCTTTACGGTAAACGGCTCCCTCAACGGC 145  
 DB 1 ATGGCCCGTGGCTGACGCTCTGCTCGCTCTCTTTACGGTAAACGGCTCCCTCAACGGC 60  
 QY 146 TGCACGCTGGCTGGCGGCTGGCGGCTGGCGGCGCGGGCGCGGACACCTGTGGC 205  
 DB TGCACGCTGGCTGGCGGCTGGCGGCTGGCGGCGCGGGCGCGGACACCTGTGGC 120  
 QY 206 TGGAGGATGAAGCGGCTGCCCGACCGCGCTTGTGTCTAATGAGGAGTGGGGCA 265  
 DB TGGAG-----GGGAGTGGGGCA 138  
 QY 266 GCCACGAGAACAGTGGGCTGTACACATCACCTTCAATATGACAAATGTACACCTAC 325  
 DB GCCACGAGAACAGTGGGCTGTACACATCACCTTCAATATGACAAATGTACACCTAC 198  
 QY 326 TTGAATCCAGTGGGGAAGCATGTGATGTGTGACGCCGAGAAATATCACCATCAGCAGTAT 385  
 DB TTGAATCCAGTGGGGAAGCATGTGATGTGTGACGCCGAGAAATATCACCATCAGCAGTAT 258  
 QY 386 GCTTCCCATGACCAAGTGGCAGTACCATCTTGTGTCGCCAGGGGCGCTGGCATCGAA 445  
 DB GCTTCCCATGACCAAGTGGCAGTACCATCTTGTGTCGCCAGGGGCGCTGGCATCGAA 318  
 QY 446 TTCCTGAAAGGATTCGGGTAACTAGTGGAGGCTGAACTGGGGAAGACAGTCCCAA 505  
 DB TTCCTGAAAGGATTCGGGTAACTAGTGGAGGCTGAACTGGGGAAGACAGTCCCAA 378  
 QY 506 CAACGTATCTAAAGGATCCGAGCAGCTCAACAGTACCTTCAAAAGCACTGGAATGAA 565  
 DB CAACGTATCTAAAGGATCCGAGCAGCTCAACAGTACCTTCAAAAGCACTGGAATGAA 438  
 QY 566 TCTCAACCTTCTCGAATATGAATTTGAACGGATATTTCTGTAAGGTTGTCCCTTTT 625  
 DB TCTCAACCTTCTCGAATATGAATTTGAACGGATATTTCTGTAAGGTTGTCCCTTTT 498  
 QY 626 CTTCCATTAAGGAAAGCAATACCACTTCTTTTCTTTAGAACCGAGCTGTGAC 685  
 DB CTTCCATTAAGGAAAGCAATACCACTTCTTTTCTTTAGAACCGAGCTGTGAC 558  
 QY 686 CTGTTGTTACAGCGGCAATCTAGCTTGTAAACCTTCTGGAAGCTCGGAACCTGAAC 745  
 DB CTGTTGTTACAGCGGCAATCTAGCTTGTAAACCTTCTGGAAGCTCGGAACCTGAAC 618  
 QY 746 ATCAGCCAGCATGGCTGGACATGACAGTGTCTTTCGACCATGACCCGCAACATTCGCG 805  
 DB ATCAGCCAGCATGGCTGGACATGACAGTGTCTTTCGACCATGACCCGCAACATTCGCG 678  
 QY 806 TTCCTTTTCTATCTTCACTACAGCTCAAGCAGGAAGCACTTTCAGGCAAGAGCC 865  
 DB TTCCTTTTCTATCTTCACTACAGCTCAAGCAGGAAGCACTTTCAGGCAAGAGCC 738  
 QY 866 TGAAGCAGGAGCAATACAGAGACGACAGCTGCTCTTCAAAATGTTTCTCCAGGG 925  
 DB TGAAGCAGGAGCAATACAGAGACGACAGCTGCTCTTCAAAATGTTTCTCCAGGG 798  
 QY 926 GATTATATATGAGCTGGTGGATGACACTACACAAAGAAAGTGTGATTTAGCC 985  
 DB GATTATATATGAGCTGGTGGATGACACTACACAAAGAAAGTGTGATTTAGCC 858

QY 986 TTAAGCCAGTGCACCTCCCGTGGCGCGGCCCATCAGAGCCGTGGCCATCAGTGGCA 1045  
 DB TTAAGCCAGTGCACCTCCCGTGGCGCGGCCCATCAGAGCCGTGGCCATCAGTGGCA 918  
 QY 1046 CTGCTAGTCAATATCGGCAATTCGGAGCGCTCTTCACTGTGATGTGGCGAAGAACAA 1105  
 DB CTGCTAGTCAATATCGGCAATTCGGAGCGCTCTTCACTGTGATGTGGCGAAGAACAA 978  
 QY 1106 GAAATATATATTCACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTCGACA 1165  
 DB GAAATATATATTCACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTCGACA 1038  
 QY 1166 CTCCCAAGAGAGAGCTCCCGCGCGCGCGGAAGCTCTTCTGCTATTCCAGTAAGAT 1225  
 DB CTCCCAAGAGAGAGCTCCCGCGCGCGCGGAAGCTCTTCTGCTATTCCAGTAAGAT 1098  
 QY 1226 GCCCAGAAATCACAATGATGCTCCAGTGTTCGCTTCTTCCAGGACTTCTGTGGC 1285  
 DB GCCCAGAAATCACAATGATGCTCCAGTGTTCGCTTCTTCCAGGACTTCTGTGGC 1158  
 QY 1286 TGTGAGTGGCTCTGGAACCTGTGGGAAGACTTCAAGCTCTGTAGAGAGGCGCAGAGAA 1345  
 DB TGTGAGTGGCTCTGGAACCTGTGGGAAGACTTCAAGCTCTGTAGAGAGGCGCAGAGAA 1218  
 QY 1346 TGGGTCAATCCAGAAATCCACAGTCCCAAGTTCATCATTTGTTTTCCTCAAGGTATG 1405  
 DB TGGGTCAATCCAGAAATCCACAGTCCCAAGTTCATCATTTGTTTTCCTCAAGGTATG 1278  
 QY 1406 AAGTACTTGTGGACAAGAGAACTTACAAACAAAGAGAGTGGCGAGGCTCGGGGAAA 1465  
 DB AAGTACTTGTGGACAAGAGAACTTACAAACAAAGAGAGTGGCGAGGCTCGGGGAAA 1338  
 QY 1466 GGAGAGCTCTTCTGCTGGCGGTGTACGCCATTCGCCAAGCTCCGCCAGGCCAAGCAG 1525  
 DB GGAGAGCTCTTCTGCTGGCGGTGTACGCCATTCGCCAAGCTCCGCCAGGCCAAGCAG 1398  
 QY 1526 AGTTGTCGCGCGCTCAGCAAGTTTATCCCGCTTACTTTGATTATTCCTCGAGGGA 1585  
 DB AGTTGTCGCGCGCTCAGCAAGTTTATCCCGCTTACTTTGATTATTCCTCGAGGGA 1458  
 QY 1586 GACGTCCCGGTATCTTACAGCTGAGTACCAAGTACAGACTCATGGACAATC-TTCCTCA 1644  
 DB GACGTCCCGGTATCTTACAGCTGAGTACCAAGTACAGACTCATGGACAATC-TTCCTCA 1518  
 QY 1645 GCTCTGTTCCTCACT-TGCCTCCGAGACACAGGCTCCAGGAGCGGGGCA-GCACAG 1702  
 DB GCTCTGTTCCTCACTCTGCCTCCGAGACACAGGCTCCAGGAGCGGGGCAATGCACAG 1578  
 QY 1703 CGACAGGGCA-GCAGAGGAACTTCTCCGAGCAAGTCAAGCGGTCTCTATAGTCGC 1761  
 DB CGACAGGGCA-GCAGAGGAACTTCTCCGAGCAAGTCAAGCGGTCTCTATAGTCGC 1638  
 QY 1762 CATTTGCAACATGCACAGTTTATTGACAGAGCGCGAGTGTTCGAAAGAGTTCGT 1821  
 DB CATTTGCAACATGCACAGTTTATTGACAGAGCGCGAGTGTTCGAAAGAGTTCGT 1698  
 QY 1822 TCCCTTCCATCTCTTCCCACTCGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGG 1881  
 DB TCCCTTCCATCTCTTCCCACTCGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGG 1758  
 QY 1882 CTTGTTTAAATGATGTGTGCAACAGGCGCTGAGAGTACTTCTGCTTAAAGGT 1941  
 DB CTTGTTTAAATGATGTGTGCAACAGGCGCTGAGAGTACTTCTGCTTAAAGGT 1818  
 QY 1942 AGAGCGGCTGTTTCTTGGGCAACCGGACAGCGACTCCCGCAGCAGAGTCAAGTGG 2001  
 DB AGAGCGGCTGTTTCTTGGGCAACCGGACAGCGACTCCCGCAGCAGAGTCAAGTGG 1878  
 QY 2002 GGGCTCGACCAAGAGCGGGAGCGCGGCTTGCCTTTGAGGTTAGCGCGCCCTCAACC 2061  
 DB GGGCTCGACCAAGAGCGGGAGCGCGGCTTGCCTTTGAGGTTAGCGCGCCCTCAACC 1938







Db 662 CGATGGCTCGGACATGAGGTGCTTCGACACGACCGACCAACTTCGGCTTCGGT 721  
QY 813 TCTTCTATCTTCACTACAGCTCAAGCAGAGGACCTTTCAAGCGAAGACCTGTAAAGC 872  
Db 722 TCTTCTATCTTCACTACAGCTCAAGCAGAGGACCTTTCAAGCGAAGACCTGTAAAGC 781  
QY 873 AGGACCAACTACAGACGACGACCTGCTCTTCAAAATGTTCTCCAGGGGATATA 932  
Db 782 AGGACCAACTACAGACGACGACCTGCTCTTCAAAATGTTCTCCAGGGGATATA 841  
QY 933 TAATTGAGTGGTGTGATGACACTAACACAAAGAAAGTGTGATCATTTATGCCCTTAAAGC 992  
Db 842 TAATTGAGTGGTGTGATGACACTAACACAAAGAAAGTGTGATCATTTATGCCCTTAAAGC 901  
QY 993 CAGTGCACCTCCCGTGGGCGGCGCCATCAGAGCGCTGGCTTCACAGTCCCACTGTAG 1052  
Db 902 CAGTGCACCTCCCGTGGGCGGCGCCATCAGAGCGCTGGCTTCACAGTCCCACTGTAG 961  
QY 1053 TCATATCGGCATTCGCGACGCTTTCACCTGTGATGCGCGAAGAACCAAGAAATA 1112  
Db 962 TCATATCGGCATTCGCGACGCTTTCACCTGTGATGCGCGAAGAACCAAGAAATA 1021  
QY 1113 TATATTACATTTAGATGAAGAGCTCTGAGTCTTCCACATACACTGCAGACTCCCAA 1172  
Db 1022 TATATTACATTTAGATGAAGAGCTCTGAGTCTTCCACATACACTGCAGACTCCCAA 1081  
QY 1173 GAGAGAGCTCGGCGGCGGCGAGGCTTTCTGTGTATTCAGTAAAGATGGCCAGA 1232  
Db 1082 GAGAGAGCTCGGCGGCGGCGAGGCTTTCTGTGTATTCAGTAAAGATGGCCAGA 1141  
QY 1233 ATCATGATGAATGCTGCTGAGTCTTCCGCTACTTCTCCAGAGCTCTGTGGCTGTAGG 1292  
Db 1142 ATCATGATGAATGCTGCTGAGTCTTCCGCTACTTCTCCAGAGCTCTGTGGCTGTAGG 1201  
QY 1293 TGGCTCTGGACCTTGGGAAGACTTCAGGCTCTGTAGAGAGGCGCAGAGATGGGTCA 1352  
Db 1202 TGGCTCTGGACCTTGGGAAGACTTCAGGCTCTGTAGAGAGGCGCAGAGATGGGTCA 1261  
QY 1353 TCCAGAAGATCCAGAGTCCAGTTCATCATTTGTGTTTGTTCGAAAGGTATGAAGTACT 1412  
Db 1262 TCCAGAAGATCCAGAGTCCAGTTCATCATTTGTGTTTGTTCGAAAGGTATGAAGTACT 1321  
QY 1413 TTGTGCAAGAAGAACTACAAACAAAGAGGCTGGCGAGGCTCGGGAAGAGAGGAC 1472  
Db 1322 TTGTGCAAGAAGAACTACAAACAAAGAGGCTGGCGAGGCTCGGGAAGAGAGGAC 1381  
QY 1473 TCTTCTGGTGGGCTGTCAGCCATTCGCGAAAGCTCCGCGAGGCGCAAGAGTTCGT 1532  
Db 1382 TCTTCTGGTGGGCTGTCAGCCATTCGCGAAAGCTCCGCGAGGCGCAAGAGTTCGT 1441  
QY 1533 CCGCGGCGCTCAGCAAGTTTATCGCGCTTACTTTGATTATTCCTGCGAGGAGAGTCC 1592  
Db 1442 CCGCGGCGCTCAGCAAGTTTATCGCGCTTACTTTGATTATTCCTGCGAGGAGAGTCC 1501  
QY 1593 CCGGTATCTAGACTGAGTACCAAGTACAGACTCATGCAATCTTCTCAGCTCTGTT 1652  
Db 1502 CCGGTATCTAGACTGAGTACCAAGTACAGACTCATGCAATCTTCTCAGCTCTGTT 1561  
QY 1653 CCCACTTCCACTCCCGAGACAGGGCTCCAGGAGCGGGGCGCAGCACACCGCAGGCGCA 1712  
Db 1562 CCCACTTCCACTCCCGAGACAGGGCTCCAGGAGCGGGGCGCAGCACACCGCAGGCGCA 1621  
QY 1713 GCAGAGGAAGTACTTCCGAGCAGTACAGGCGGCTTCCCTATAGTCCCATTTGCAACA 1772  
Db 1622 GCAGAGGAAGTACTTCCGAGCAGTACAGGCGGCTTCCCTATAGTCCCATTTGCAACA 1681  
QY 1773 TGCACAGTTTATTGACGAGAGCCGAGTGTTCGAAAGCAGTTTCCTTCCCTTCCATC 1832  
Db 1682 TGCACAGTTTATTGACGAGAGCCGAGTGTTCGAAAGCAGTTTCCTTCCCTTCCATC 1741  
QY 1833 CTCCTCCACTCGGTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1892  
Db 1742 CTCCTCCACTCGGTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1801

QY 1893 ATGATGTCATGTGCAAAACAGGGCTGAGAGTCTTCTGCTAAAGGTAGAGGGCGGTG 1952  
Db 1802 ATGATGTCATGTGCAAAACAGGGCTGAGAGTCTTCTGCTAAAGGTAGAGGGCGGTG 1861  
QY 1953 TTCTTGGGCAACCGGACAGCGGAGTCCAGCAGAGAGTCCAGATGGGGCTTGGACC 2012  
Db 1862 TTCTTGGGCAACCGGACAGCGGAGTCCAGCAGAGAGTCCAGATGGGGCTTGGACC 1921  
QY 2013 AAGACGGGGAGGGCCGCGCTTTCAGCGTAGCGCGCCCTGCAACCCCTGCTGCACA 2072  
Db 1922 AAGACGGGGAGGGCCGCGCTTTCAGCGTAGCGCGCCCTGCAACCCCTGCTGCACA 1981  
QY 2073 CGGTGAAGCGCGCAGCCCTCGGACATGCCGCGGACTCAGGCATCTATGACTGCTGTG 2132  
Db 1982 CGGTGAAGCGCGCAGCCCTCGGACATGCCGCGGACTCAGGCATCTATGACTGCTGTG 2041  
QY 2133 TGCCCTCATCCGAGCTGTCTCTGCCACTGTGGAAGGACTTCGACGAGCAGACAGAAA 2192  
Db 2042 TGCCCTCATCCGAGCTGTCTCTGCCACTGTGGAAGGACTTCGACGAGCAGACAGAAA 2101  
QY 2193 CGTCTTCCCTGACGAGAGGCTGCTCTCTTCAGCGCTGGGTGAGGAGAACCTCTGTG 2252  
Db 2102 CGTCTTCCCTGACGAGAGGCTGCTCTCTTCAGCGCTGGGTGAGGAGAACCTCTGTG 2161  
QY 2253 CCCTTCCCTTCCAGCTCTCTCTTCGCGTATGCAAGCAGATCTTGGTTCGCGAGCT 2312  
Db 2162 CCCTTCCCTTCCAGCTCTCTCTTCGCGTATGCAAGCAGATCTTGGTTCGCGAGCT 2221  
QY 2313 ACACGTGATGAATCCAGCGGCTGGCCCTTTGTAAACAAAACAGAGTCTAAGCATTCG 2372  
Db 2222 ACACGTGATGAATCCAGCGGCTGGCCCTTTGTAAACAAAACAGAGTCTAAGCATTCG 2281  
QY 2373 CACTTTA 2379  
Db 2282 CACTTTA 2288  
RESULT 8  
ABA95037  
ID ABA95037 standard; DNA; 2443 BP.  
XX ABA95037;  
AC ABA95037;  
XX 20-MAY-2002 (first entry)  
DT 20-MAY-2002 (first entry)  
XX Murine cytokine receptor, zcytor18 nucleotide sequence.  
DE Cytokine receptor; zcytor18; cell proliferation; antiproliferative; human;  
KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
KW erythroleukemia; chromosome 3p14.3; gene therapy; mouse; ds.  
XX Mus sp.  
XX Key Location/Qualifiers  
FH CDS 101..2320  
FT /\*tag= a  
FT /product= "mouse zcytor18"  
XX WO200208259-A2.  
PN 31-JAN-2002.  
PD 23-JUL-2001; 2001WO-US23253.  
PF 26-JUL-2000; 2000US-220747P.  
PR (ZYMO) ZYMOGENETICS INC.  
XX Presnell SR, Kuestner RE, Gao Z;  
XX WPI; 2002-217048/27.  
DR P-PSDB; ABB07630.







PS Disclosure; Page 101-102; 119pp; English.

XX The invention relates to an isolated cytokine receptor polypeptide designated Zcytor18. The Zcytor18 polypeptides can be expressed by standard recombinant methodology. The polypeptides can be used to inhibit cell proliferation associated with psoriasis or tumour growth. The encoding nucleic acids are useful for providing Zcytor18 in vivo by gene therapy techniques. Zcytor18 oligonucleotide probes are useful for in vivo diagnosis, and the Zcytor18 probes and primers can be used to detect and localize Zcytor18 gene expression in tissue samples. The probes are also useful for detecting gross aberrations in chromosome 3 in which Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in linkage-based testing of pulmonary alveolar proteinosis, familial peridiotic fever and erythroleukemia, and erythroleukemia associated with polymorphisms of cytokine receptors. The present sequence represents a human Zcytor18 variant degenerate coding sequence.

XX Sequence: 2259 BP; 379 A; 234 C; 374 G; 293 T; 979 other;

Query Match 57.6%; Score 1612; DB 24; Length 2259;  
Best Local Similarity 56.6%; Pred. No. 0;  
Matches 1278; Conservative 576; Mismatches 404; Indels 0; Gaps 0;

QY 86 ATGGCCCGGCTGGCGAGCTCTGCTCGCTCTCTTTAGGTCACAGCTCCCTCAACGGC 145  
DB 1 ATGGCCCGGCTGGCGAGCTCTGCTCGCTCTCTTTAGGTCACAGCTCCCTCAACGGC 60

QY 146 TCGCAGCTGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCG 205  
DB 61 WNCARYTNGCNGTNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG 120

QY 206 TGGAGGATGAAGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCG 265  
DB 121 TGGAGGATGAAGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCG 180

QY 266 GCGCAGCAGAGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGG 325  
DB 181 GCGCAGCAGAGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGGCGGCTGG 240

QY 326 TTGAATCAGTGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 385  
DB 241 TTAATCAGTGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300

QY 386 GCTTCCATGACCAAGTGGCGAGTCAACATCTTGTGCTCCCGAGGGGCTCGGCGATCGAA 445  
DB 301 GCTTCCATGACCAAGTGGCGAGTCAACATCTTGTGCTCCCGAGGGGCTCGGCGATCG 360

QY 446 TTCCTGAAGGATTCGGGTATATCTGGAGGAGTGAAGTGGAGGAGGAGGAGGAGGAGG 505  
DB 361 TTTTGAAGGATTCGGGTATATCTGGAGGAGTGAAGTGGAGGAGGAGGAGGAGGAGG 420

QY 506 CAACATGATCTTAAGGATTCGGGTATATCTGGAGGAGTGAAGTGGAGGAGGAGGAGG 565  
DB 421 CAACATGATCTTAAGGATTCGGGTATATCTGGAGGAGTGAAGTGGAGGAGGAGGAG 480

QY 566 TCTCAACCTTCCTGAATGATGAATTTGAACGGATTTATCTGAAGGTTGTCCTTTT 625  
DB 481 WNCARCCNTTTCCTGAATGATGAATTTGAACGGATTTATCTGAAGGTTGTCCTTTT 540

QY 626 CTTCCATTAATAAGCAAGCAATATACACCTCTCTCTTTAGAACCCGAGCTGTGAC 685  
DB 541 CTTCCATTAATAAGCAAGCAATATACACCTCTCTCTTTAGAACCCGAGCTGTGAC 600

QY 686 CTGTGTGTACAGCGGCAATCTAGCTGTAAACCTCTTCGAGGCTCGGAGCTCGGAGCTGA 745  
DB 601 TTTTGTGTGTACAGCGGCAATCTAGCTGTAAACCTCTTCGAGGCTCGGAGCTCGGAG 660

QY 746 ATCAGCAGCTGGCTGGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 805  
DB 661 ATCAGCAGCTGGCTGGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 720

QY 806 TTCCGCTTCTTCTATCTTCTATCTTCTATCTTCTATCTTCTATCTTCTATCTTCTATCT 865  
DB 1801 GTTNTAAYGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860

DB 721 TTYNGTTTTTYYTTCATYATYATYATYATYATYATYATYATYATYATYATYATYAT 780

QY 866 TGTAAAGCAGGAGCAAACTACAGAGCAGCAGCTCTCTCTCTCTCTCTCTCTCTCTCT 925

DB 781 TGTAAAGCAGGAGCAAACTACAGAGCAGCAGCTCTCTCTCTCTCTCTCTCTCTCTCT 840

QY 926 GATTAATATATTCAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 985

DB 841 GATTAATATATTCAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 900

QY 986 TTAAGCCAGTGCATCCCGCTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1045

DB 901 YTNAAACCCNTCAAYNSCCNTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 960

QY 1046 CTGTGTATCATATCGCATCTCGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1105

DB 961 YTNGTGTATATTCAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1020

QY 1106 GAAATATATATTCAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1165

DB 1021 GAAATATATATTCAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1080

QY 1166 TCCCAAGAGAGAGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1225

DB 1081 YTNCCNGGAGAGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140

QY 1226 GCGCAGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1285

DB 1141 GCGCAGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200

QY 1286 TGTGAGTGGCTCTGAGGAGCTGTGAGGAGCTGTGAGGAGCTGTGAGGAGCTGTGAGG 1345

DB 1201 TGTGAGTGGCTCTGAGGAGCTGTGAGGAGCTGTGAGGAGCTGTGAGGAGCTGTGAG 1260

QY 1346 TGGGTATCAGCAGAGATCCAGAGTCCAGTTCATCTGATGATGATGATGATGATGATG 1405

DB 1261 TGGGTATCAGCAGAGATCCAGAGTCCAGTTCATCTGATGATGATGATGATGATGATG 1320

QY 1406 AAGTACTTCTTGACAAAGAACTACAAACAAAGAGAGTGGCGGAGCTCGGCGGAGAA 1465

DB 1321 AAGTACTTCTTGACAAAGAACTACAAACAAAGAGAGTGGCGGAGCTCGGCGGAGAA 1380

QY 1466 GGAGAGCT 1525

DB 1381 GGAGAGCT 1440

QY 1526 AGTTCGTCGCGGCGCTCAGAGTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1585

DB 1441 WSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSN 1500

QY 1586 GACCTCCCGGATTCCTAGACCTGAGTACCAAGTACAGAGCTCATGACAGTCTCTCTC 1645

DB 1501 GAYTNCNGGAGTTCATCT 1560

QY 1646 CTCGTTCCTCCAGTTCAGTCCGAGCAGCAGCTCCAGGAGCGGCGGCGGCGGCGG 1705

DB 1561 YTNGTGTATATTCAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1620

QY 1706 CAGGCGCAGCAGAGAGTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1765

DB 1621 CAGGCGCAGCAGAGAGTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1680

QY 1766 TGCAGATGACAGCAGTTCATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1825

DB 1681 TGCAGATGACAGCAGTTCATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740

QY 1826 TCCATCT 1885

DB 1741 TTYCAYCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 1800

QY 1886 GTTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1945

DB 1801 GTTNTAAYGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860







Query Match 62.8%; Score 1496; DB 24; Length 2214;  
 Best Local Similarity 54.7%; Pred. No. 0;  
 Matches 1236; Conservative 566; Mismatches 411; Indels 45; Gaps 2;

QY 86 ATGGCCCGGTGGGTGAGCTCTGCTCCGCTCTCTTTACGCTCAACGCTCCGCTCAACGCG 145  
 DB 1 ATGCNCCGCTGGTTCARTTGTGWSNGTNTTYYACNGTNAAYGCTGYTNAAYG 60

QY 146 TCGCAGTGGCTGTGGCGCTCGCGGCTCGCGGCGCGGCGCGGCGGCGGCGGCGGCGG 205  
 DB 61 WSNCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

QY 206 TGGAGGATGAACGGCTGCCGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265  
 DB 121 TGG-----NNNGGCTGNGCNCN 138

QY 266 GCCAGCAGAACAGTGGGCTGTACACATCACTTCAATATGACAAATGTACCACTAC 325  
 DB 139 GCHNSMGNAAYSNGGNTTAYAAATACNTTAAATAYGAYAAATGYACNATAY 198

QY 326 TTGAATCCAGTGGGAGCATGCTGCTGACGCCGAGATATACCATCAGCCAGTAT 385  
 DB 199 YTNAYCNGTNGNNAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 258

QY 386 GCTTGGCATGACCAAGTGGCAGTCACTTCTTGGTCCGAGGCGCTCGGCAATGAA 445  
 DB 259 GCNTGYCAYGAYCARGTNGCNGTACNATHYTNTGWSNCGGCGCTGCTGCTGCTGCTGCTG 318

QY 446 TTCCTGAAGAGATTTCGGTAAATCTGCGAGGCTGAAGTGGGAGGAGAGAGAGCGCAA 505  
 DB 319 TTYTNAARGNTTYMGCTNATHYTNGARGARTNAARNSARGNGNGCNRNNCR 378

QY 506 CACTGATCTTAAGGATCGGAGCGCTCAACAGTACGCTTCAAAAGAACTCGAATGAA 565  
 DB 379 CARYTNATHYTNAARGAYCCNARCNNAAYSNSTTYAARMGACNGGATGAR 438

QY 566 TCTCAACCTTCTCTGAATGAATTTGAAACGAGTATTTCTGTAAGGCTTCTCCTTTT 625  
 DB 439 WSNCAACNNNTTAAATGAARTTYGARACNAYTATYTGCTN- --GNTWNSNTTY 495

QY 626 CTTTCCATTAACACAGCAATTAACACGCTTCTTTTGAACCGGAGCTGTGAC 685  
 DB 496 WSNTHAARAYGARNSAAYTAYCAYCCNTTCTTTTGMNACNGGCTGYGAY 555

QY 686 CTGTGTTACAGCGGCAATCTAGCTTGTAAACCTTCTGGAAGCGCTCGGAACCTGAAC 745  
 DB 556 YTNNTNTNCAACGAYAAAYTNGCTGYAARCNNTTYGGAARCNMNAAYTNAAY 615

QY 746 ATCAGCCAGCATGCTCGACATGAGGCTGCTTCCAGCATCCAGCGACACACTTCGC 805  
 DB 616 ATHSNCAATGAGGNGAYATGARGTNSNTTYGAYCNCNCAAYAYTYG 675

QY 806 TTCGGTCTTCTATCTTCACTAAGCTCAAGCAGGAGCTTCAAGCGAAAGAAC 865  
 DB 676 TTYMGNTTCTTAYTAYTAYTAYTAYTAYTAYTAYTAYTAYTAYTAYTAYTAYTAYTAYTAY 735

QY 866 TGAAGCAGGAGAACTACAGAGACGAGCTGCTTCCAAATCTTCTCCAGG 925  
 DB 736 TGYAARCARCARACACNACNARATGACNWSNTTYTNTNCARAYGTWNSCNGN 795

QY 926 GATTATATATGAGCTGGTGGATGACACTAACACAAAGAAAGTATGATATGCC 985  
 DB 796 GATTATATATGAGCTGGTGGATGACACTAACACAAAGAAAGTATGATATGCC 855

QY 986 TTAAGCCAGTGCCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1045  
 DB 856 YTNARCCGCTNAYSNCCNTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 915

QY 1046 CTGTTAGTATATGCGCATTCGCGAGCTCTTCACTGCTGATGTCGCGGAGAGCAACAA 1105  
 DB 916 YTNGTNGTNAHWSNCGNTTTCNACNTTNTTYACNGTNTATGTYMGNAARAARCAR 975

QY 1106 GAAATATATATTCACATTTAGATGAAGAGAGCTCTGAGCTCTTCCACATACACTCGACA 1165  
 DB 976 GAAAT 1035

QY 1166 CTCCCAAGAGAGAGCTCG 1225  
 DB 1036 YTNCCNMGNGARGMNTNMGNCNMGNCNMGNCNMGNCNMGNCNMGNCNMGNCNMGNCNMG 1095

QY 1226 GCGCAGATACATGAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1285  
 DB 1096 GGCARAAATCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1155

QY 1286 TGTAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1345  
 DB 1156 TGTAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1215

QY 1346 TGGCTCATCCAGAGATCCAGAGTCCAGTTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1405  
 DB 1216 TGGCTNATCCARAAATCAATGAGTTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1275

QY 1406 AGCTACTTTGTGCAAGAGAGTACAAACAAAGAGTGGCGGAGCTCGCGGAA 1465  
 DB 1276 AATATATTTGTGTAARAAAT 1335

QY 1466 GGAGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1525  
 DB 1336 GNGAATTTTNTTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNG 1395

QY 1526 AGTCTGCTGCGCGGCTGCAAGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1585  
 DB 1396 WSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWS 1455

QY 1586 GAGTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1645  
 DB 1456 GAYTNCNCGNATHYTNGAYTNGAYTNGAYTNGAYTNGAYTNGAYTNGAYTNGAYTNGAYT 1515

QY 1646 CTCTGTTCCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1705  
 DB 1516 YTNWYNSCAATTCAYWNSMNGAYCAYGNTNARGCNGCNGCNGCNGCNGCNGCNGCNGC 1575

QY 1706 CAGGCGCAGCAGAGAGTACTTCTGCGAGCAGTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 1765  
 DB 1576 CAGGCGCAGCAGAGAGTACTTCTGCGAGCAGTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 1635

QY 1766 TCGAATCATCCAGCTTTATGAGGAGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1825  
 DB 1636 TGYAATGAYCATTTATGAGGAGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1695

QY 1826 TCCATCTCTCTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1885  
 DB 1696 TTYCATCCMCCMCCMCCMCCMCCMCCMCCMCCMCCMCCMCCMCCMCCMCCMCCMCCMCCMCC 1755

QY 1886 GTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1945  
 DB 1756 GTTYTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1815

QY 1946 GCGGCTGCTTCTGCGGCAACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2005  
 DB 1816 GCGGCTGCTTCTGCGGCAACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1875

QY 2006 CTGAGCAAGAGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2065  
 DB 1876 YTNAGCAGGAGGAGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1935

QY 2066 CTCACACGCTGAAAGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2125  
 DB 1936 YTNCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1995

QY 2126 TCGCTG 2185  
 DB 1996 WSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWSNWS 2055

QY 2186 ACAGAAACCTCTTCTCTGAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2245







252	AGGAGTGGGGCAGCCAGCGAAGAACAGTGGCGGTGTACACATCACCTTCAAAATATGACA	311
220	AGGAGTGGGGCAGCGAAGAACAGTGGCGGTGTACACATCACCTTCAAAATATGACA	279
312	ATTGTACCACTACTTGAATCCAGTGGGGAAGCATGTGATGCTGAGGCCAGGAATATCA	371
280	ATTGTACCACTACTTGAATCCAGTGGGGAAGCATGTGATGCTGAGGCCAGGAATATCA	339
372	CAATCAGCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATCTTTGGTCCCCAGGGG	431
340	CCATCAGCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATCTTTGGTCCCCAGGGG	399
432	CCCTCGGCATCGAATTCCTGGAAGGATTTCCGGGTAACTACTGGAGAGCTGAATCGGAGG	491
400	CCCTCGGCATCGAATTCCTGGAAGGATTTCCGGGTAACTACTGGAGAGCTGAATCGGAGG	459
492	GAAGACAGTGGCCAAACAACCTGATTTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA	551
460	GAAGACAGTGGCCAAACAACCTGATTTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA	519
552	GAACCTGGAATGGAATCTCAACCTTCTCTGTAATATGAATTTCAACCGATATTTCTGTA	611
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612	AGTTGTCCCTTTCTCTCCATTAACCAAGAAAGCAATTACACCTTTCTTCTTTAGAA	671
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672	CCCGAGCCTGTGACCTGTGTTGTACAGCGGACAACTAGCTTGTAAACCTTCTGGAAGC	731
640	CCCGAGCCTGTGACCTGTGTTGTACAGCGGACAACTAGCTTGTAAACCTTCTGGAAGC	699
732	CTCGGAACCTGAAACATCAGCAGCATGGCTCGCAGATGCGAGGTGCTTTCGACCATTGCAC	791
700	CTCGGAACCTGAAACATCAGCAGCATGGCTCGCAGATGCGAGGTGCTTTCGACCAGCAC	759
792	CGCACAACTTCGCGTTTCGGTTTCTTCTATCTTCACCTACAAGCTCAAGCAGGAAGACCTT	851
760	CGCACAACTTCGCGTTTTCGGTTTCTTCTATCTTCACCTACAAGCTCAAGCAGGAAGACCTT	819
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972	TGATGCATTATGCTTTAAAGC	992

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QY 1404 TGAAGTACTTGTGGACAAGAACTACAACACAAAGAGGTGGCCGAGGCTCGGGGA 1463  
Db 1444 CGCGCGCAAGTGGCAGGCGCTCTGGGCGCGGGGGCGCTGTGCGGCTGCGCTCGGACC 1503  
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QY 1764 TTTGCAACATGCACCAAGTTTATGACGAGAGCCCGACTGTTTCGAAAGCAGTTTCGTT 1823  
Db 1804 TGGACAGGTTCCGGGACTGGCAGGTCCGCTGTCCCGACTGGTTCGAATGTGAGAACCTCT 1863  
QY 1824 CCT 1826  
Db 1864 ACT 1866

Search completed: May 12, 2003, 21:13:08  
Job time : 374 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 10:35:26 ; Search time 2245 Seconds  
(without alignments)  
17191.022 Million cell updates/sec

Title: US-09-912-157-1

Perfect score: 2383

Sequence: 1 cgcgcgcgcaccccccac.....aaacattccacttagctg 2383

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*\*  
1: em\_estba:\*\*  
2: em\_esthum:\*\*  
3: em\_estin:\*\*  
4: em\_estnu:\*\*  
5: em\_estov:\*\*  
6: em\_estov:\*\*  
7: em\_estpl:\*\*  
8: em\_estro:\*\*  
9: gb\_est1:\*\*  
10: gb\_est2:\*\*  
11: gb\_est3:\*\*  
12: gb\_est4:\*\*  
13: gb\_est5:\*\*  
14: gb\_est6:\*\*  
15: em\_estfun:\*\*  
16: em\_estom:\*\*  
17: gb\_gss:\*\*  
18: em\_gss\_hum:\*\*  
19: em\_gss\_inv:\*\*  
20: em\_gss\_pln:\*\*  
21: em\_gss\_vit:\*\*  
22: em\_gss\_fun:\*\*  
23: em\_gss\_mam:\*\*  
24: em\_gss\_mus:\*\*  
25: em\_gss\_other:\*\*  
26: em\_gss\_pro:\*\*  
27: em\_gss\_rod:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	453.6	19.0	649	10	BB616055
2	433	18.2	665	10	BB641245
3	431	18.1	547	12	BE750478
4	375.8	15.8	390	9	AA778029
5	351.8	14.8	377	12	BF803798
6	325.6	13.7	627	10	AW645591

7	325.2	13.6	577	12	BG721995
8	318.2	13.4	680	10	BB263921
9	304.4	12.8	705	9	AL728651
10	300.4	12.6	1010	14	BQ734807
11	263	11.0	485	10	AW646237
12	260.8	10.9	813	13	BG985616
13	253	10.6	323	14	BQ306217
14	247.4	10.4	526	12	BF615262
15	238	10.0	636	13	BG985614
16	237.4	10.0	448	10	BE679435
17	233.4	9.8	614	13	BI987186
18	229.8	9.6	584	9	AL650928
19	211.8	8.9	585	12	BI987186
20	205	8.6	659	10	BB616562
21	204.8	8.6	478	13	BQ306217
22	192.8	8.1	541	10	AW641445
23	189.2	7.9	230	12	BF515598
24	184.2	7.7	856	10	BE470523
25	183.8	7.7	545	9	AL777282
26	172.4	7.2	827	13	BG985833
27	167.2	7.0	730	13	BI987186
28	161.4	6.8	411	10	AW767446
29	150.6	6.3	698	17	BH066762
30	150.2	6.3	424	10	AW766603
31	148.4	6.2	291	10	BB288874
32	131	5.5	398	9	AI088588
33	128.6	5.4	539	10	AW233052
34	127	5.3	796	17	AO780842
35	121.4	5.1	494	10	AW233130
36	119.8	5.0	633	13	BI988786
37	117.4	4.9	596	14	BQ450534
38	103	4.3	806	13	BG985617
39	100	4.2	520	17	BH091008
40	89	3.7	563	13	BQ39747
41	89	3.7	644	13	BQ307093
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43	85.8	3.6	682	9	AV274569
44	84.8	3.6	496	17	FR0025211
45	79	3.3	284	17	FR0018488

## ALIGNMENTS

RESULT 1  
BB616055  
LOCUS  
DEFINITION  
BB616055 RIKEN full-length enriched, adult male testis Mus musculus  
CDNA clone 4931403M23.5', mRNA sequence.  
ACCESSION  
BB616055  
VERSION  
BB616055.1 GI:16456248  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus.  
REFERENCE  
1 (bases 1 to 649)  
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kudo, M., Koye, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
EST. 26-OCT-2001

TITLE  
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
JOURNAL  
Unpublished (2001)  
COMMENT  
Contact: Yoshinori Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216









JOURNAL  
MEDLINE  
COMMENT

sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000).  
20202663

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-C10075-  
021100-003-c02&t3=2000-11-02&t4=1)

Seq primer: puc18 forward  
High quality sequence stop: 377.  
Location/Qualifiers  
1..377

## FEATURES

source  
1..377  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="C10075"  
/dev\_stage="Adult"  
/note="Organ: colon\_lns; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 106 a 98 c 87 g 86 t

Query Match 14.8%; Score 351.8; DB 12; Length 377;  
Best Local Similarity 99.4%; Pred. No. 2.5e-81;  
Matches 353; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 891 CGACAGCTGCTCTTCAAAATGTTCTCCAGGGATTATATATGACCTGGTGATG 950  
DB 23 CGACAGCTGCTCTTCAAAATGTTCTCCAGGGATTATATATGACCTGGTGATG 82  
QY 951 ACACATACACACAGAAAGTATGATTCATTCCTTAAGCCAGTGCCTCCCTGGG 1010  
DB 83 ACACATACACACAGAAAGTATGATTCATTCCTTAAGCCAGTGCCTCCCTGGG 142  
QY 1011 CCGGCCCATCAGAGCGCTGGCCATCAGAGTGCCTAGTATGATTCGGCATTCGCGA 1070  
DB 143 CCGGCCCATCAGAGCGCTGGCCATCAGAGTGCCTAGTATGATTCGGCATTCGCGA 202  
QY 1071 CGCTTTCACATGATGTCGCGAAGACACAGAAATATATATTCACATTTAGATG 1130  
DB 203 CGCTTTCACATGATGTCGCGAAGACACAGAAATATATATTCACATTTAGATG 262  
QY 1131 AGAGAGCTGATGCTTCACATACATGACAGTGCCTCCAGAGAGAGCTCCGCCCGC 1190  
DB 263 AGAGAGCTGATGCTTCACATACATGACAGTGCCTCCAGAGAGAGCTCCGCCCGC 322  
QY 1191 GCGCGAGGCTTCTCTGCTATTCAGTAAAGATGGCCAGATCATCATGATGT 1245  
DB 323 GCGCGAGGCTTCTCTGCTATTCAGTAAAGATGGCCAGATCATCATGATGT 377

RESULT 6  
LOCUS  
AW645591 627 bp mRNA linear EST 26-APR-2001  
DEFINITION  
cm34f07.wl.blackshear/Soares normalized Xenopus egg library Xenopus  
laevis cDNA clone PBX015f07 5', mRNA sequence.  
ACCESSION  
AW645591  
VERSION  
AW645591.1 GI:7403045  
KEYWORDS  
EST.  
SOURCE  
Xenopus laevis  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT

Amphibia: Batrachia; Anura; Mesobatrachia; Pipidae;  
Xenopodinae; Xenopus.  
1 (bases 1 to 627)  
Blackshear,P.J.; Lai,W.S.; Thorn,J.M.; Kennington,E.A.; Staffa,N.G.  
Jr.; Moore,D.T.; Bouffard,G.G.; Beckstrom-Sternberg,S.M.; Touchman  
J.W.; Bonaldo,M.F. and Soares,M.B.  
The NIHES Xenopus maternal EST project: interim analysis of the  
first 13,879 ESTs from unfertilized eggs  
Gene 267 (1), 71-87 (2001)  
21211403

Contact: Perry J. Blackshear  
Office of Clinical Research and Laboratory of Signal Transduction  
National Institute of Environmental Health Sciences  
AL-05, NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,  
USA  
Tel.: 919-541-4899;  
Fax: 919-541-4571  
Email: black009@niehs.nih.gov  
Clone is available through Research Genetics, Inc., 2130 Memorial  
Parkway, Huntsville, AL 35901  
phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email  
cdna@resgen.com  
DNA Sequencing and analyses performed by National Institutes of  
Health Intramural Sequencing Center (NISC).  
PCR Primers  
FORWARD: TGTAAGACAGCGGCGAGT  
BACKWARD: CAGGAACAGCTATGACC  
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Seq primer: T7 primer.

## FEATURES

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/cell\_type="unfertilized egg"  
/dev\_stage="unfertilized egg"  
/lab\_host="DH10B"

/note="Vector: pT73-Pac; Site\_1: EcoRI; Site\_2: NotI;  
PolyA-selected mRNA was prepared from unfertilized Xenopus  
laevis eggs. The library was constructed in the vector  
pT73-Pac as described in Bonaldo, M.F., Lennon, G. and  
Soares, M.B. 'Normalization and subtraction: two  
approaches to facilitate gene discovery', Genome Research  
6:791-806, 1996. The first strand synthesis used a  
NotI-dri18 primer; double stranded cDNAs were ligated to  
EcoRI adapters, digested with NotI, and directionally  
cloned into the NotI and EcoRI-digested pT73-Pac vector.  
The library contained approximately 7.2 x 10<sup>5</sup>  
recombinants, with average insert sizes of 1-1.5 kb."

BASE COUNT 172 a 159 c 153 g 143 t  
ORIGIN

Query Match 13.7%; Score 325.6; DB 10; Length 627;  
Best Local Similarity 70.3%; Pred. No. 2.6e-74;  
Matches 436; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

QY 269 AGCAGAACAGTGGGCTGTACACATCACCTTCAATATATGACAAATTTGACCACTTGT 328  
DB 3 AGCAGAACACCGGGCTGCCCAATGTCCACTTACGATATGACAACTGCCTTCATG 62  
QY 329 ATCCAGTGGGGAGAGCTGTCTGCGCCAGATATACCATCAGCAGCATGTCT 388  
DB 63 ACCCAGAGGAGGACACCAAGATTTGGGATGTACAGACATATACGTCAGTTCCTCC 122  
QY 389 TGCCATGACCAAGTGGCAGTCACCATTTCTTTGGTCCCGAGGGCCCTCGGCATCAATTC 448  
DB 123 TGCAACAGCAAGTGGCGGTCTGTCTCTGCGAGCGCAATGATATATCGGCATCAATAC 182  
QY 449 CTGGAAGGATTTCCGGTATATCTAGGAGGCTGAAGTCGGAGGGAGACAGACAGTGCACCA 508

Db 183-CTGAAGGCTTCGGGTGCTGGTGAAGAGCTCAAGTCCGAGGGCGGATTCGTGACAA 242  
 QY 509-CTGATCTAAGGATCCGAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGAATCT 568  
 Db 243-ATGGTGATGAGGATCCGAGCAGCTCAAGTGAAGTCAAAAGAGTTGTAATGGAATCT 302  
 QY 569-CAACCTTCTGATGAATGAATTTGAACGAGTATTTGTAAGAGTTGTCCTTTTCCT 628  
 Db 303-CAGCGGTATCAACTGAATTTGAACAGAGTATTTGTAAGAGTTGTCCTTTTCCT 362  
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 Db 363-TCCGCCCAAGTAAGTAATACCACTCTCTCTCTCAGGAGCCGACCTGTGAGTCT 422  
 QY 689-TTGTACAGCCGAGCAATCTAGCTGTAAACCTTCTGGAAGCTCTGGAACCTGAACATC 748  
 Db 423-TTGTGACCCGAGCAGTCTGACCTCGAGCCATCTGGAACCAAAAGAGTCAAGCTC 482  
 QY 749-AGCAGAGGCTCGGACATCAGCTGCTCTCGACCATGCAACGACCACTTCGGCTTC 808  
 Db 483-ACCAACAGGGCTCAACATCAGCTGCTCTTTGACCGGCGCCCTCGGAATTTTCGGTTT 542  
 QY 809-CGTTTCTTCTATCTTCACTACAACTCAACGACGAGGAGCTTCAACGAGAGACCTGT 868  
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 QY 869-AACGAGGAGCAACTACAGA 888  
 Db 603-CGCAGGCTCTGAACACGGA 622

RESULT 7  
 LOCUS BG721995 577 bp mRNA linear EST 08-MAY-2001  
 DEFINITION 602498761f1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:4830807 5',  
 mRNA sequence.

ACCESSION BG721995

VERSION EST

KEYWORDS EST

SOURCE human

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshitsugu and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLNL10752 row: 1 column: 16  
 High quality sequence stop: 576.

FEATURES

1..577

Location/Qualifiers

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/db\_xref="taxon:9606"

/clone="IMAGE:4830807"

/clone\_lib="NIH\_MGC\_97"

/lab\_host="DH10B"

/note="Organ: testis; Vector: pBluescriptR (modified  
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 normalized to R05. This is a primary library enriched  
 for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library  
 constructed by M. Brownstein (NHGRI/NHRI, National  
 Institutes of Health). Note: this is a NIH\_MGC Library.  
 BASE COUNT 155 a 136 c 166 g 120 t  
 ORIGIN

Query Match 13.6%; Score 325.2; DB 12; Length 577;

Best Local Similarity 92.4%; Pred. No. 3.2e-74;

Matches 353; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

QY 208 GAGGATGAAGCGCTCCCGACCCGGCTTTGTCTTAATGAGGAGTGGGGCAGC 267

Db 196 GTGGCTGAAGCTGTGACTGACCTACAGGCAATCTGGCTTGGCAGGAGTGGGGCAGC 255

QY 268 CAGCAGAAAGCTGGCTGTGACCAATCACTTCAAAATATGACAAATTTGTACCACTTCT 327

Db 256 CAGCAGAAAGCTGGCTGTGACCAATCACTTCAAAATATGACAAATTTGTACCACTTCT 315

QY 328 GAATCCAGTGGGGAAGCATGTGATCTGACGCCAGCAATATCACCATCAGCAGTATGC 387

Db 316 GAATCCAGTGGGGAAGCATGTGATCTGACGCCAGCAATATCACCATCAGCAGTATGC 375

QY 388 TTGCCATGACCAAGTGGCAGTCACTTCTTTGGTCCCGAGGCGCTCGGCATCGAAT 447

Db 376 TTGCCATGACCAAGTGGCAGTCACTTCTTTGGTCCCGAGGCGCTCGGCATCGAAT 435

QY 448 CTGAAA-GGATTTCCGGTAAATCTGGAGGAGCTGAAGTCCGAGGAGAGACAGTGCAC 506

Db 436 CTGAAAAGGATTTCCGGTAAATCTGGAGGAGCTGAAGTCCGAGGAGAGACAGTGCAC 495

QY 507 AACTGATTCTAAAGTCCGAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGAAT 566

Db 496 AACTGATTCTAAAGTCCGAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGAAT 555

QY 567 CTCACCTTTCTCTGAATATGAA 588

Db 556 CTCACCTTTCTCTGAATATGAA 577

RESULT 8

LOCUS BB263921 680 bp mRNA linear EST 24-OCT-2001

DEFINITION BB263921 RIKEN full-length enriched, 10 days neonate cortex Mus

ACCESSION BB263921

VERSION BB263921.2 GI:16400169

KEYWORDS EST

SOURCE house mouse

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,  
 Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda,  
 M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ono, M.,  
 Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki,  
 D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,  
 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,  
 Muramatsu, M. and Hayashizaki, Y.

TITLE RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

JOURNAL Unpublished (2001)

COMMENT On Jul 7, 2000 this sequence version replaced gi:8960377.  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@sc.riken.go.jp  
 URL: <http://genome.gsc.riken.go.jp/>  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh,  
 M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.



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QY 1065 TCAGGAGCTTCTACTGTGATGGCGCAGAGCAACAGAAATATATATATTCACATT 1124
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 263 TCAGGAGCTTCTACTGTGATGGCGCAGAGCAACAGAAATATATATATTCACACC 322
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1125 TAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCAAGAGAGGCTCC 1184
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 323 TGACGAGGAGAGCTCGAGTCTTCTATCCGACACACAGCTCTGAGCGCAGAGACCT 382
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1185 GCGCGCGCGGAGAGTCTTCTCTGCTATTCAGTAAGATGGCGCAGATCATCATGATG 1244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 383 GCGCGCGAGCCCAAAATCTTCATCTGTACTCCAGCAGAGAGGAGCCAAACACCTCGCG 442
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1245 TCCTCAGTGTTCGCTTACTTCTCCAGGACTTCTGTGGCTGTGAGGTGGCTCTGGACC 1304
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 443 TCATCCAGAGCTTCGCTTCTCTCTGCGAGGACTTCTGCGGAGCGAGGTTCTCTGGACC 502
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1305 TGTGGGAGACTTCAGCTCTGTAGAGAGAGGCGCAGAGAGTGGTCTATCCAGAGATCC 1364
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Db 503 TCTGGGAGCCTGGAGATCTGTAGAGAGGTCAGATCTCTGTGGTGGCGGCGCATCG 562
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1365 ACAGTCCAGTTCATCATTTGTTGTTTCCAAAGGTATGAAGTACTTTTGTGGACAAGA 1424
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Db 563 ACAGAGCCACTTCATCATCAGCTGTCTCCAAAGGCTGAAACACTTGTGGAGAAAC 622
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QY 1425 AGAATCTACAAACACAAAG 1442
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Db 623 GCCAGCCCAAGGCAAG 640
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RESULT 10
BQ734807
LOCUS
DEFINITION BQ734807 1010 bp mRNA linear EST 16-JUL-2002
AGENCOURT 8510861 NICHDR XGC Emb4 Xenopus laevis cDNA clone
IMAGE:4684214 5', mRNA sequence.
ACCESSION BQ734807
VERSION BQ734807.1 GI:21873704
KEYWORDS EST
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 1010)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnli.gov/brp/image/image.html
Plate: LHAM10568 row: m column: 15
High quality sequence stop: 428.
Location/Qualifiers
1. .1010
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:4684214"
/clone.lib="NICHDR XGC Emb4"
/dev_stage="embryo, stage 31-32"
/note="Host-DH10B (phage-resistant)"
/note="Organ: whole embryo; Vector: pCMV-Sport6; Site: 1.
NotI; Site: 2. SalI; Cloned unidirectionally. Primer: Oligo
db. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC
) library."
249 a 319 c 240 g 202 t

FEATURES
source

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Query Match 12.6%; Score 300.4; DB 14; Length 1010;
Best Local Similarity 70.5%; Pred. No. 1.5e-67;
Matches 443; Conservative 0; Mismatches 181; Indels 4; Gaps 3;

QY 825 ACTACAGCTCAAGCAGAGAGACCTTTCAAGCCGAAGAGACTGTAAAGCAGGAGCAACTA 884
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 19 ACTACAACCTGAAGCAGAGAGGCTCTTTAAACAGAGAGATCTCCGGAAGGTCGTGAACA 78
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 885 CAGAGAGCAGCAGCTGCTCTCTTCAAAATGTTCTCCAGGGGATTATATAATTGAGCTGG 944
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Db 79 CAGACTTCACCAACTGCTGATCCAGAAAGTATCCCGGGGAGCTATGTCATAGAGCTG 138
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 945 TGGATGACACTAACACAAACAGAAAGTGTGATTCATTTGCTTAAAGCCAGTGCATCCC 1004
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Db 139 TGGAGCAGACACACAGCAGAGAGTTCATGCACTACTGCTGGAACACAGTGCATTCCT 198
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QY 1005 COTGGCGCGGCGCCATCAGAGCGGTGGCCATCAGCAGTGCACCTAGTATCATATCGCAT 1064
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Db 199 CTGGCGCGGTCCCAATACAGCCCATCGCCCTACTGTACCCCTGGTCATCATATCTGCT 258
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1065 TCGCGAGCGCTCTTCACTGTGTGTCGCGCAAGAAAGCAAGAAATATATATTCACATT 1124
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 259 TGGCCACTTTATTACCGTCTCATGTGCGCAAGAGCAGCAAGAACATTTACTCGCAC 318
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1125 TAGATGAAGAGAGCTGTGAGTCTTCCATATACACTGCAGCCTCCCAAGAGAGAGGCTCC 1184
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Db 319 TGGAGCAGAGAGAGTTCGGAATCATCTACCTACGAGGAGTCTTCAAGTGGAGAGAGCC 378
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1185 GCGCGCGCGGAGAGTCTTCTCTGCTATTCCAGTAAAGATGGCCAGATCATCATGAATG 1244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 379 GCGCGCGCGCGGAGTCTTCTCTGCTACTCCACTAAAGATTGTCAGAGAGCATTATG 438
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1245 TCGTCCAGTCTTTCGCTACTTCTCTCAGGACTTCTGCTGCTGTGA-GTGGCTCTGCAC 1303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 439 TCATCCACTCTTTCGCTATTCTCTGAGGATTTCTGTGGTCCAGGGTTTCGCTGGAT 498
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QY 1304 CTGTGGGAGACTTCAGCCTCTGTAGAGAGGCGCAGAGAGTGGGT--CATCCAGAGA 1361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 499 CTCTGGGAGAACCTGAAAGATCTGTAAGCAGCGCCGCGAGTGGCTTGGAAACCAAGA 558
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1362 TCCAGAGTCCCAAGTTCATCATTTGTTGTTTCCAAAGGTATGAAGTACTTTT-GTGAC 1420
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Db 559 TCCAGATTCCCACTACATCACCCTGCTGCTCCAGGCTCTCCAACTACTTTTGTGGAC 618
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QY 1421 AAGAGAACTACAAACACAAAGAGGTG 1448
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Db 619 AGGAAATGGAAGCCACAAAGGGGG 646
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RESULT 11
AM646237 485 bp mRNA linear EST 26-APR-2001
LOCUS AM646237
DEFINITION ch2605.w1 Blackshear/Soares normalized Xenopus egg library Xenopus
laevis cDNA clone PBX0161805 5', mRNA sequence.
ACCESSION AM646237
VERSION AM646237.1 GI:7403719
KEYWORDS EST
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 485)
Blackshear,P.J., Lai,W.S., Thorn,J.M., Kennington,E.A., Staffa,N.G.
Jr., Moore,D.T., Bouffard,G.G., Beckstrom-Sternberg,S.M., Touchman
J.W., Bonaldo,M.F. and Soares,M.B.
The NIEHS Xenopus maternal EST project: Interim analysis of the
first 13,879 ESTs from unfertilized eggs
Gene 267 (1), 71-87 (2001)
21211403
JOURNAL
MEDLINE
COMMENT
Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction

```

National Institute of Environmental Health Sciences  
A2-05 NIBES, 101 Alexander Drive, Research Triangle Park, NC 27709,  
USA

Tel: 919 541-4899

Fax: 919 541-4571

Email: black009@niehs.nih.gov

Clone is available through Research Genetics, Inc., 2130 Memorial

Parkway, Huntsville, AL 35901

phone 800-533-4363 ext. cdna, fax 256-536-9016 att:cdna, email

cdna@resgen.com

DNA Sequencing and analyses performed by National Institutes of

Health Intramural Sequencing Center (NISC).

PCR Primers

FORWARD: TGTAACACGCGCCGCT

BACKWARD: CAGGAACAGTATGACC

Plate: 0161 row: E column: 05

Seq primer: T7 primer.

Location/Qualifiers

1. 485

/organism="Xenopus laevis"

/db\_xref="taxon:8355"

/clone="PBX0161E05"

/clone\_lib="Blackshear/Soares normalized Xenopus egg

library"

/sex="female"

/tissue\_type="unfertilized egg"

/cell\_type="unfertilized egg"

/dev\_stage="unfertilized egg"

/lab\_host="DH10B"

/notes="Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI;

PolyA-selected mRNA was prepared from unfertilized Xenopus

laevis eggs. The library was constructed in the vector

pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and

Soares, M.B. 'Normalization and subtraction: two

approaches to facilitate gene discovery', Genome Research

6:791-806, 1996. The first strand synthesis used a

NotI-dT18 primer; double stranded cDNAs were ligated to

EcoRI adapters, digested with NotI, and directionally

cloned into the NotI and EcoRI-digested pT7T3-Pac vector.

The library contained approximately 7.2 x 10<sup>5</sup>

recombinants, with average insert sizes of 1-1.5 kb."

BASE COUNT 135 a 116 c 123 g 111 t

ORIGIN

Query Match 11.0%; Score 263; DB 10; Length 485;

Best Local Similarity 72.4%; Pred. No. 6.6e-58;

Matches 341; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 269 AGCAGAACAGTGGCTGTACACATCACCTTCAATATGACATTTGACCACCTACTTG 328

DB 15 AGCAGAACACCGGGTGGCCATGTCCTTACATATGACATTTGACCTGCTTATG 74

QY 329 AATCAGTGGGAGCATGTGATGTGTCAGCCGACCAATATCACCATCAGCAGTATGCT 388

DB 75 AACCCAGGAGGAGGACGACCATGTGGGATGTACAGAACATACGTCAGTCTGTC 134

QY 389 TGCCATGACCAAGTGGGAGTGCACCATCTTGTGTCGCCGCGCCCTCGGCATCGAATTC 448

DB 135 TGCACAGCAGCAAGTGGGGGTCTCTGCTCTGGACGGCCATGATATTCGGCATCGAATAC 194

QY 449 CTGAAGGATTTGGGTGTAATCTAGGAGGAGCTGAAGTGGGAGGAGGAGACAGTGCACAA 508

DB 195 CTGAAGGCTTTCGGGTGGTGGTGGAGAGCTGAAGTGGGAGGAGGAGTCTGTACAG 254

QY 509 CTGATTTCTAAAGGATCGAAGGAGCTCAACAGTACCTTCAAGAGACTGGAATGAACT 568

DB 255 ATGGTGATGAAGATCCAGCAGCTGATGTGACCTTCAAGAGTGTGATGGAATCT 314

QY 569 CAACCTTCTGATATGAATTTGAACGGGATATTTCTGTAAGGTGTGCTCTTCTCT 628

DB 315 CAGCGGTTTATCACTTGAATTTGAACAGATTTATTTGCAAAATTTGTGCTTTTCC 374

QY 629 TCCATTAAACAGGAACCAATTACACCTTCTTCTTTAGAACCCGCGCTGTGACCTG 688

DB 375 TCCGCCAGAAATGAAGTATTACATCCGTTCTTTCAGGACCGCCACTGTGAGTCT 434

QY 689 TTGTTACAGCCGACCAATCTAGCTTTGTAACCCCTTCTGGAAGCTCGGAAC 739

DB 435 TTGTTGAGCGACAGCTGTGACCTGCGAGCCATCTGGAACCAACAAAC 485

RESULT 12

LOCUS BG985616 813 bp mRNA linear EST 13-JUN-2001

DEFINITION 5059f1 NICHD zebrafish normalized 1 Danio reflo cDNA clone 5059,

mRNA sequence.

ACCESSION BG985616

VERSION BG985616.1 GI:14389696

KEYWORDS EST

SOURCE zebrafish.

ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes

; Cyprinidae; Danio

REFERENCE 1 (bases 1 to 813)

AUTHORS Kudoh, T., Tsang, M., Hukriede, N.A., Chen, X., Dedekian, M., Clarke

, C.J., Kiang, A., Schultz, S., Epstein, J.A., Toyama, R. and David, I.B.

A gene expression screen in zebrafish embryogenesis

Genome Res. 11 (12), 1979-1987 (2001)

JOURNAL 21588053

MEDLINE Other ESTs: 5059t3, 5059t7, 5059r1

COMMENT Contact: David IB

Laboratory of Molecular Genetics

National Institute of Child Health and Human Development, NIH

Bldg 6B, Room 413, 9000 Rockville Pike, Bethesda, MD 20892 USA

Tel: 301 496 4448

Fax: 301 496 0243

Email: idavid@nih.gov

Seq primer: Fl.

Location/Qualifiers

1. 813

/organism="Danio rerio"

/db\_xref="taxon:7955"

/clone="5059"

/clone\_lib="NICHD zebrafish normalized 1"

/dev\_stage="bud to 10 somite stage embryos"

/note="Vector: pBluescript KS+; Site 1: NotI; Site 2: SalI

; RNA was reverse-transcribed to first strand cDNA using

SuperScriptII reverse-transcriptase and tagged oligo-dT

primer which contains several restriction sites including

a NotI site:

gactgtcttagatcgatcgagcggccggccgcccccttttttttttt. Second

strand DNA was synthesized by E. coli DNA polymerase I in

combination with E. coli RNase H and E. coli DNA ligase.

Double stranded cDNA was ligated with SalI adapter. These

cDNAs were cloned into the SalI/NotI site of pBluescript

KS+ and transformed into E. coli Electromax DH10B by

electroporation.

BASE COUNT 205 a 257 c 193 g 158 t

ORIGIN

Query Match 10.9%; Score 260.8; DB 13; Length 813;

Best Local Similarity 70.4%; Pred. No. 3.4e-57;

Matches 349; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 947 GATCAGACTAACCAACAAGAAAGTATGATGATATGCTTAAAGCAGTCCACTCCCG 1006

DB 6 GATCAGAGCAACACACAGAGACGAGCGATATCAGCTCAGCAATTCATCTCCG 65

QY 1007 TGGCGCCGGGCCCCATCAGACCCGTGCGCATACATGCGCACTGTGATGATCGCATTC 1066

DB 66 TGGCGCCGGGCGGATCGTGGCCATCCATCCGCTCCGCTGATCATGTCAGCGCTTC 125

QY 1067 GCGACGCTCTTCACTGTGATGTGCGCGCAAGCAACAAATAATATATTCACATTTA 1126

DB 126 GCGCACTCTTCACTGTGATGTGCGCGCAAGCAACAAACATCTACTCTCCTG 185









GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

# OM protein protein search, using sw model

Run on: May 6, 2003, 13:34:21 ; Search time 43 seconds  
(without alignments)  
2333.435 Million cell updates/sec

Title: US-09-912-157-2

Perfect score: 4013

Sequence: 1 MAPWQLCSVFTVNAACLG ..... CQADLCGRSYDELHNAVPL 753

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A\_Geneseq\_1010022.\*

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6:	/SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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21:	/SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4013	100.0	753	23	Human cytokine rec
2	4003	99.8	753	23	Human cytokine rec
3	3925	97.8	739	23	Human cytokine rec
4	3501	97.2	738	22	Human Interleukin
5	3897	97.1	738	22	Human Interleukin
6	3896	97.1	738	22	Human Interleukin
7	3894	97.0	738	22	Human Interleukin
8	3894	97.0	738	22	Human Interleukin
9	3894	97.0	738	22	Human Interleukin
10	3890	96.9	738	22	Human Interleukin

11	3890	96.9	738	22	AAU09957	Human Interleukin
12	3830.5	95.5	738	23	AAU11355	Human DNAX cytokin
13	3703	92.3	728	22	AAU04958	Human Interleukin
14	3703	92.3	739	22	AAU10602	Human Interleukin
15	3387	84.4	739	23	ABB07630	Murine cytokine re
16	2699.5	67.3	554	23	AAU91330	Human novel secret
17	1337	33.3	296	22	AAU10601	5' portion of Huma
18	312	7.8	866	17	AAW04185	Human Interleukin-
19	312	7.8	866	19	AAW61272	Human Interleukin-
20	312	7.8	866	20	AAW92409	Human IL-17R prote
21	312	7.8	866	21	AAV99941	Human IL-17R prote
22	312	7.8	866	21	AAV97131	Human Interleukin-
23	312	7.8	866	21	AAV97181	Human Interleukin-
24	312	7.8	866	21	AAW03807	Human Interleukin-
25	312	7.8	866	22	AAW62086	Human IL-17R (HCL
26	312	7.8	866	22	AAW72754	Human Interleukin
27	306	7.6	864	17	AAW04184	Mouse Interleukin
28	306	7.6	864	19	AAW61271	Murine IL-17R prot
29	306	7.6	864	20	AAW92408	Murine IL-17R prot
30	306	7.6	864	21	AAV99935	Murine Interleukin
31	306	7.6	864	21	AAV97130	Murine Interleukin
32	306	7.6	864	21	AAV97180	Murine Interleukin
33	306	7.6	864	21	AAW03806	Murine IL-17R poly
34	306	7.6	864	22	AAW62080	Murine Interleukin
35	306	7.6	864	22	AAV72748	Human IL-17 recept
36	271.5	6.8	539	23	AAW47457	Human IL-17RH matu
37	135.5	3.4	238	20	AAV31624	Human secreted pro
38	135.5	3.4	385	21	AAW25795	Human secreted pro
39	135.5	3.4	385	22	AAW75381	Human IL-17 recept
40	135.5	3.4	385	23	AAW47459	Human PRO polypept
41	135.5	3.4	502	22	AAU29223	Human EST encoded
42	135.5	3.4	502	22	AAW24349	Human Interleukin
43	135.5	3.4	502	22	AAU04955	Human protein havi
44	135.5	3.4	502	22	AAE06586	Human PRO5801. Ho
45	135.5	3.4	502	22	AAW87604	

## ALIGNMENTS

### RESULT 1

ABB07626  
ID ABB07626 standard; Protein; 753 AA.

AC ABB07626;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, zcytor18 amino acid sequence.

XX Cytokine receptor; zcytor18; cell proliferation; antiproliferative; human;  
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;  
KW erythroleukemia; chromosome 3p14.3; gene therapy.

OS Homo sapiens.

PN WO200208259-A2.

PD 31-JAN-2002.

PF 23-JUL-2001; 2001WO-US23253.

PR 26-JUL-2000; 2000US-220747P.

PA (ZYMO) ZYMOGENETICS INC.

PI Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

DR N-PSDB; ABA95031, ABA95032.

XX New cytokine receptor polypeptide designated zcytor18, useful for

PT inhibiting cell proliferation associated with psoriasis or tumor

PT growth, and modulating immune system by binding to endogenous zcytor18  
 Pt ligand  
 PS Claim 1; Page 2; 119pp; English.  
 XX The invention relates to an isolated cytokine receptor polypeptide  
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by  
 CC standard recombinant methodology. The polypeptides can be used to inhibit  
 CC cell proliferation associated with psoriasis or tumor growth. The  
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
 CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in  
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
 CC and localize zcytor18 gene expression in tissue samples. The probes are  
 CC also useful for detecting gross aberrations in chromosome 3 in which  
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
 CC linkage-based testing of pulmonary alveolar proteinosis, familial  
 CC periodic fever and erythroleukemia, and erythroleukemia associated with  
 CC polymorphisms of cytokine receptors. The present sequence represents a  
 CC human zcytor18 amino acid sequence.  
 XX Sequence 753 AA:

Query Match 100.0%; Score 4013; DB 23; Length 753;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPWLQCSVFFTVNACLSGSLAVAAGSGRARGADTCGRWKAARPRCLVANEVGP 60  
 Db 1 MAPWLQCSVFFTVNACLSGSLAVAAGSGRARGADTCGRWKAARPRCLVANEVGP 60  
 QY 61 ASRNSGLYNTFFDYNTCTILNPVGRVIAQAQNTISQYACHQDVAVTILWSPGALGIE 120  
 Db 61 ASRNSGLYNTFFDYNTCTILNPVGRVIAQAQNTISQYACHQDVAVTILWSPGALGIE 120  
 QY 121 FLGFRVILEELKSEGRQCOQLILKDPKLNSEFKRGESOPFLNMFETDVFVKVVPF 180  
 Db 121 FLGFRVILEELKSEGRQCOQLILKDPKLNSEFKRGESOPFLNMFETDVFVKVVPF 180  
 QY 181 PSIKNESNYHPPFRTRACDILLQPDNLACKPFWKPRNLNISOHSDMQVDFDAPINFG 240  
 Db 181 PSIKNESNYHPPFRTRACDILLQPDNLACKPFWKPRNLNISOHSDMQVDFDAPINFG 240  
 QY 241 FRFFYLHYKLKHEGPPKRTCKEQTTTSCLLQNVSPGYIIELVDDTNTTKRVHYA 300  
 Db 241 FRFFYLHYKLKHEGPPKRTCKEQTTTSCLLQNVSPGYIIELVDDTNTTKRVHYA 300  
 QY 301 LKPVHSPWAGPIRAVAITVPLVLSAFATLFTVCKKQOENIYSHLDEESSESTYTA 360  
 Db 301 LKPVHSPWAGPIRAVAITVPLVLSAFATLFTVCKKQOENIYSHLDEESSESTYTA 360  
 QY 361 LPRERLRPRKPVLCYSSKQDNHNVVQCFAYFLQDFGCEVALDLMEDFSLCREGORE 420  
 Db 361 LPRERLRPRKPVLCYSSKQDNHNVVQCFAYFLQDFGCEVALDLMEDFSLCREGORE 420  
 QY 421 WVIQKHESQFIIVVCSKGMKVFYDKNRYKHGSGRGSGELFLVAVSAEKLRAQK 480  
 Db 421 WVIQKHESQFIIVVCSKGMKVFYDKNRYKHGSGRGSGELFLVAVSAEKLRAQK 480  
 QY 481 SSSAALSKEFIATVDFYSCGDDVPGILDLSTKYRLMNLPLQCLSHLRDHLQEPGQTR 540  
 Db 481 SSSAALSKEFIATVDFYSCGDDVPGILDLSTKYRLMNLPLQCLSHLRDHLQEPGQTR 540  
 QY 541 QGSRNRYFRSKGRSLIYAICNMHOFIDEPDFEKOFPVPHPPPLRYRVPVLEKPSGL 600  
 Db 541 QGSRNRYFRSKGRSLIYAICNMHOFIDEPDFEKOFPVPHPPPLRYRVPVLEKPSGL 600  
 QY 601 VLNDVCKKQPSDFCLKVAEAVLGATGAPDASQHSQHGGLDQDGEARPAALDGAALQPL 660  
 Db 601 VLNDVCKKQPSDFCLKVAEAVLGATGAPDASQHSQHGGLDQDGEARPAALDGAALQPL 660  
 QY 661 LHTVKAQSPDMRDSGIYDSSVPSSELSLPLMEGLSTDTQTTSSLTSSVSSSGLGEE 720  
 Db 661 LHTVKAQSPDMRDSGIYDSSVPSSELSLPLMEGLSTDTQTTSSLTSSVSSSGLGEE 720

OY 721 PPALPSKLLSSGCKRADIGCRSYTDELHVAAPL 753  
 Db 721 PPALPSKLLSSGCKRADIGCRSYTDELHVAAPL 753

## RESULT 2

AB07627  
 ID AB07627 standard; Protein; 753 AA.

XX AC AB07627;

XX DT 20-MAY-2002 (first entry)

XX DE Human cytokine receptor, zcytor18 variant sequence.

XX KW Cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human;  
 XX NM pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
 XX RW erythroleukemia; chromosome 3p14.3; gene therapy; variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 269

XX FT /label= "P269M"

XX FT /note= "Wild-type Thr is replaced with Met"

XX FT Misc-difference 750

XX FT /label= "V750A"

XX FT /note= "Wild-type Val is replaced with Ala"

XX PN W0200208259-A2.

XX XX 31-JAN-2002.

XX XX 23-JUL-2001; 2001WO-US23253.

XX XX 26-JUL-2000; 2000US-220747P.

XX XX (ZYMO ) ZYMOGENETICS INC.

XX XX Presnell SR, Kuestner RE, Gao Z;

XX XX WPI; 2002-217048/27.

XX XX N-PSDB; ABA95033, ABA95034.

XX PT New cytokine receptor polypeptide designated zcytor18, useful for  
 XX PT inhibiting cell proliferation associated with psoriasis or tumor  
 XX PT growth, and modulating immune system by binding to endogenous zcytor18  
 XX PT ligand

XX PS Disclosure; Page 94-98; 119pp; English.

XX CC The invention relates to an isolated cytokine receptor polypeptide  
 XX CC designated zcytor18. The zcytor18 polypeptides can be expressed by  
 XX CC standard recombinant methodology. The polypeptides can be used to inhibit  
 XX CC cell proliferation associated with psoriasis or tumor growth. The  
 XX CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
 XX CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in  
 XX CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
 XX CC and localize zcytor18 gene expression in tissue samples. The probes are  
 XX CC also useful for detecting gross aberrations in chromosome 3 in which  
 XX CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
 XX CC linkage-based testing of pulmonary alveolar proteinosis, familial  
 XX CC periodic fever and erythroleukemia, and erythroleukemia associated with  
 XX CC polymorphisms of cytokine receptors. The present sequence represents a  
 XX CC human zcytor18 variant amino acid sequence.

XX SQ Sequence 753 AA;

Query Match 99.8%; Score 4003; DB 23; Length 753;  
 Best Local Similarity 99.7%; Pred. No. 0;

Matches 751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAPNLQCSVFTVNAACNGSOLAAGSGRAGADTCGRMKAARPRCLVANEVGP 60  
 DB 1 MAPNLQCSVFTVNAACNGSOLAAGSGRAGADTCGRMKAARPRCLVANEVGP 60  
 QY 61 ASRNSGLNITFKYDNCCTTILNPGVKHVIADAOQNTISQYACHDQVAVTILMSPGALGIE 120  
 DB 61 ASRNSGLNITFKYDNCCTTILNPGVKHVIADAOQNTISQYACHDQVAVTILMSPGALGIE 120  
 QY 121 FLKGFVILLEELKSEGRCQOOLILKDPKOLNSFKRTGMSQPFANKEFETDYFKVVPF 180  
 DB 121 FLKGFVILLEELKSEGRCQOOLILKDPKOLNSFKRTGMSQPFANKEFETDYFKVVPF 180  
 QY 181 PSIKNESNYHPFFTRACDILLQPDNLACPFKPKNLNISQSGSDMQVSDHAPHNFG 240  
 DB 181 PSIKNESNYHPFFTRACDILLQPDNLACPFKPKNLNISQSGSDMQVSDHAPHNFG 240  
 QY 241 FRFFYLHYLKHGPPFKRTCKOBTETTSCLLQNVSPGDYIIELVDDTNTTRVMHYA 300  
 DB 241 FRFFYLHYLKHGPPFKRTCKOBTETTSCLLQNVSPGDYIIELVDDTNTTRVMHYA 300  
 QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRKQENIYSHLDESSSESTYAA 360  
 DB 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRKQENIYSHLDESSSESTYAA 360  
 QY 361 LPRERLRPRKPVLCYSSKDGQNHNNVQCFAYFLQDFCGCEVALDLMEDFSLCREGORE 420  
 DB 361 LPRERLRPRKPVLCYSSKDGQNHNNVQCFAYFLQDFCGCEVALDLMEDFSLCREGORE 420  
 QY 421 WYIQRHESQFIIVVCSKGMKYFVDKKNYKHGGSGSGGELFLVAVSAIAEKLRQAKO 480  
 DB 421 WYIQRHESQFIIVVCSKGMKYFVDKKNYKHGGSGSGGELFLVAVSAIAEKLRQAKO 480  
 QY 481 SSSAALSFFIAYFDYSCGSDVPGIIDLSTKYRLMDNLPLQCSHLSDRHGLQEPQOHTR 540  
 DB 481 SSSAALSFFIAYFDYSCGSDVPGIIDLSTKYRLMDNLPLQCSHLSDRHGLQEPQOHTR 540  
 QY 541 QCSRNTFRSKSGSLYVAICNNHQFIDEEPDMFEKQFVFPHPPLRYREPVLKFDGSL 600  
 DB 541 QCSRNTFRSKSGSLYVAICNNHQFIDEEPDMFEKQFVFPHPPLRYREPVLKFDGSL 600  
 QY 601 VLNDVCKKPGESDFCLVBAVLGNTGPADSOHESQHGGLDQDGEARPALDGSALQPL 660  
 DB 601 VLNDVCKKPGESDFCLVBAVLGNTGPADSOHESQHGGLDQDGEARPALDGSALQPL 660  
 QY 661 LHTVAGSPDMPDRSGIYDSSVPSSELSLPLMGLSTDTQETSSLTSSVSSGLGEE 720  
 DB 661 LHTVAGSPDMPDRSGIYDSSVPSSELSLPLMGLSTDTQETSSLTSSVSSGLGEE 720  
 QY 721 PPALPSKLLSSGCKADLCRSYTDLHVAAPL 753  
 DB 721 PPALPSKLLSSGCKADLCRSYTDLHVAAPL 753

## RESULT 3

ABB07628

ID ABB07628 standard; Protein; 739 AA.

XX AC

XX AC

XX DT

XX 20-MAY-2002 (first entry)

XX DE

XX Human cytokine receptor, Zcytor18 splice variant.

XX DE

KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;  
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;  
 KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.

XX OS

XX Homo sapiens.

XX XX

XX WO200208259-A2.

XX XX

XX 31-JAN-2002.

XX XX

PF 23-JUL-2001; 2001WO-US23253.  
 XX 26-JUL-2000; 2000US-220747P.  
 XX (ZYMO) ZYMOGENETICS INC.  
 XX Presnell SR, Kuestner RE, Gao Z;  
 XX WPT; 2002-217048/27.  
 XX N-PSDB; ABA95035, ABA95036.  
 PT New cytokine receptor polypeptide designated zcytor18, useful for  
 PT inhibiting cell proliferation associated with psoriasis or tumor  
 PT growth, and modulating immune system by binding to endogenous zcytor18  
 PT ligand  
 XX Claim 1; Page 102-106; 119pp; English.  
 XX The invention relates to an isolated cytokine receptor polypeptide  
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by  
 CC standard recombinant methodology. The polypeptides can be used to inhibit  
 CC cell proliferation associated with psoriasis or tumor growth. The  
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene  
 CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in  
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect  
 CC and localize zcytor18 gene expression in tissue samples. The probes are  
 CC also useful for detecting gross aberrations in chromosome 3 in which  
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in  
 CC linkage-based testing of pulmonary alveolar proteinosis, familial  
 CC periodic fever and erythroleukemia, and erythroleukemia associated with  
 CC polymorphisms of cytokine receptors. The present sequence represents a  
 CC human zcytor18 splice variant.  
 SQ Sequence. 739 AA;

Query Match 97.8%; Score 3925; DB 23; Length 739;

Best Local Similarity 98.1%; Pred. No. 0;

Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MAPNLQCSVFTVNAACNGSOLAAGSGRAGADTCGRMKAARPRCLVANEVGP 60

DB 1 MAPNLQCSVFTVNAACNGSOLAAGSGRAGADTCGRMKAARPRCLVANEVGP 46

QY 61 ASRNSGLNITFKYDNCCTTILNPGVKHVIADAOQNTISQYACHDQVAVTILMSPGALGIE 120

DB 47 ASRNSGLNITFKYDNCCTTILNPGVKHVIADAOQNTISQYACHDQVAVTILMSPGALGIE 106

QY 121 FLKGFVILLEELKSEGRCQOOLILKDPKOLNSFKRTGMSQPFANKEFETDYFKVVPF 180

DB 107 FLKGFVILLEELKSEGRCQOOLILKDPKOLNSFKRTGMSQPFANKEFETDYFKVVPF 166

QY 181 PSIKNESNYHPFFTRACDILLQPDNLACPFKPKNLNISQSGSDMQVSDHAPHNFG 240

DB 167 PSIKNESNYHPFFTRACDILLQPDNLACPFKPKNLNISQSGSDMQVSDHAPHNFG 226

QY 241 FRFFYLHYLKHGPPFKRTCKOBTETTSCLLQNVSPGDYIIELVDDTNTTRVMHYA 300

DB 227 FRFFYLHYLKHGPPFKRTCKOBTETTSCLLQNVSPGDYIIELVDDTNTTRVMHYA 286

QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRKQENIYSHLDESSSESTYAA 360

DB 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRKQENIYSHLDESSSESTYAA 346

QY 361 LPRERLRPRKPVLCYSSKDGQNHNNVQCFAYFLQDFCGCEVALDLMEDFSLCREGORE 420

DB 347 LPRERLRPRKPVLCYSSKDGQNHNNVQCFAYFLQDFCGCEVALDLMEDFSLCREGORE 406

QY 421 WYIQRHESQFIIVVCSKGMKYFVDKKNYKHGGSGSGGELFLVAVSAIAEKLRQAKO 480

DB 407 WYIQRHESQFIIVVCSKGMKYFVDKKNYKHGGSGSGGELFLVAVSAIAEKLRQAKO 466

QY 481 SSSAALSFFIAYFDYSCGSDVPGIIDLSTKYRLMDNLPLQCSHLSDRHGLQEPQOHTR 540

Db 467 SSSAALSKFIAYFYDSCGDPVGLDLSKTYRLMDNLPOLCSHLSDHGLQEPQOHTR 526  
 QY 541 QGSRNNYFRSKGRSLYVAICNMHQFIDEPPDFEFKQFVFPFPPPLRYRREPVEKFDGSL 600  
 Db 527 QGSRNNYFRSKGRSLYVAICNMHQFIDEPPDFEFKQFVFPFPPPLRYRREPVEKFDGSL 586  
 QY 601 VLNDVCKPESDFCLAEVAVLGATGADSDHSHQHGGLDQGEARPAALDGSAAQLPL 660  
 Db 587 VLNDVCKPESDFCLAEVAVLGATGADSDHSHQHGGLDQGEARPAALDGSAAQLPL 646  
 QY 661 LHTVKAQSPDMRDSGIYDSSVPSSELSPLMEGLSTDTQTSLSLTSVSSSGLGEER 720  
 Db 647 LHTVKAQSPDMRDSGIYDSSVPSSELSPLMEGLSTDTQTSLSLTSVSSSGLGEER 706  
 QY 721 PPALPSKLLSSGSKADLCGRSYTDELHVAPL 753  
 Db 707 PPALPSKLLSSGSKADLCGRSYTDELHVAPL 739

## RESULT 4

AAU09904 standard; Protein: 738 AA.

XX AAU09904;

XX 14-FEB-2002 (first entry)

XX Human Interleukin 17 (hIL-17) receptor like protein.

XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human.

XX Homo sapiens.

XX W0200168859-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-US08678.

XX 16-MAR-2000; 2000US-189815P.

XX 28-NOV-2000; 2000US-0724460.

XX (AMGE-) AMGEN INC.

XX Jing S.

XX WPI; 2001-611392/70.

XX N-PSDB; AAS15346.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 PT diabetes, psoriasis and glaucoma.

XX Claim 2; Page 152-154; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anorectic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-leukemic, dermatological,  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal.

CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17rlp may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17rlp antibodies and antagonists may also be used to down regulate  
 CC expression and activity. This is the amino acid sequence of the human  
 CC Interleukin 17 (IL-17) receptor like protein described in the method of  
 CC the invention.

XX Sequence 738 AA;

Query Match. 97.2%; Score 3901; DB 22; Length 738;

Best Local Similarity 97.6%; Pred. No. 0;

Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 1 MAPWLQCSVFETVNAACGSLVAAGGSGRAGADTCGRKKAARPLCVANGVGP 60  
 Db 1 MAPWLQCSVFETVNAACGSLVAAGGSGRAGADTCGRKKAARPLCVANGVGP 60  
 QY 61 ASRNSGLNITFKYDNCNTTYLNPVGHVIAADQNTITISQACHDQVAVTILWSPGALGTE 120  
 Db 47 ASRNSGLNITFKYDNCNTTYLNPVGHVIAADQNTITISQACHDQVAVTILWSPGALGTE 106  
 QY 121 FLKGRVILELSEKSGRQCQQLILKDPKLNSSFRKTKMESQPLNKKFTDYFVAVVVF 180  
 Db 107 FLKGRVILELSEKSGRQCQQLILKDPKLNSSFRKTKMESQPLNKKFTDYFVAVVVF 166  
 QY 181 PSIKNSNYHPFFRRACDLILQDNLNACKPFWKPRNLNISQHGSDQVSDFAHPNFG 240  
 Db 167 PSIKNSNYHPFFRRACDLILQDNLNACKPFWKPRNLNISQHGSDQVSDFAHPNFG 226  
 QY 241 FRFFYLHYKLKHEGPFKRTCKQEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 300  
 Db 227 FRFFYLHYKLKHEGPFKRTCKQEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 286  
 QY 301 LKPVHSPWAGPIRAVATVPLVVISAFATLFTVWCKKQENIYSHLDESSSESTYTA 360  
 Db 287 LKPVHSPWAGPIRAVATVPLVVISAFATLFTVWCKKQENIYSHLDESSSESTYTA 346  
 QY 361 LPRERLRPRKVFCLYSSKDGQNHNVVQCFAFLQDFGCGEVALDWEFSLCREGORE 420  
 Db 347 LPRERLRPRKVFCLYSSKDGQNHNVVQCFAFLQDFGCGEVALDWEFSLCREGORE 406  
 QY 421 WYIOKIHESQFIIVCVSKGMKYFVDKKNYKHGGRSGGKELFLVAVSAIAEKLRAQK 480  
 Db 407 WYIOKIHESQFIIVCVSKGMKYFVDKKNYKHGGRSGGKELFLVAVSAIAEKLRAQK 466  
 QY 481 SSSAALSXFIATVFDYSCGDPVGLDLSKTYRLMDNLPOLCSHLSDHGLQEPQOHTR 540  
 Db 467 SSSAALSXFIATVFDYSCGDPVGLDLSKTYRLMDNLPOLCSHLSDHGLQEPQOHTR 526  
 QY 541 QGSRNNYFRSKGRSLYVAICNMHQFIDEPPDFEFKQFVFPFPPPLRYRREPVEKFDGSL 600  
 Db 527 QGSRNNYFRSKGRSLYVAICNMHQFIDEPPDFEFKQFVFPFPPPLRYRREPVEKFDGSL 586  
 QY 601 VLNDVCKPESDFCLAEVAVLGATGADSDHSHQHGGLDQGEARPAALDGSAAQLPL 660  
 Db 587 VLNDVCKPESDFCLAEVAVLGATGADSDHSHQHGGLDQGEARPAALDGSAAQLPL 646  
 QY 661 LHTVKAQSPDMRDSGIYDSSVPSSELSPLMEGLSTDTQTSLSLTSVSSSGLGEER 720  
 Db 647 LHTVKAQSPDMRDSGIYDSSVPSSELSPLMEGLSTDTQTSLSLTSVSSSGLGEER 706  
 QY 721 PPALPSKLLSSGSKADLCGRSYTDELHVAAP 752  
 Db 707 PPALPSKLLSSGSKADLCGRSYTDELHVAAP 739

DB 707:PPALPSKLLSSGCKADLCGRSYTDELHAVAP 738

# RESULT 5:

ID AAU09953 standard; Protein: 738 AA

XX AC AAU09953;

XX 14-FEB-2002 (first entry)

DE Human Interleukin-17 (hIL-17), receptor like protein substitution #3.

KW Interleukin-17; hIL-17 receptor like protein, immunomodulatory;  
anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
mutin.

XX Homo sapiens

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 363 /label= Ser, Thr, Ala, Cys

XX WO200168859-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-US08678.

XX 16-MAR-2000; 2000US-189816P.

XX 28-NOV-2000; 2000US-0724460.

XX (ANGE-) AMGEN INC.

XX Jing S;

XX WPI; 2001-611392/70.

XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,  
useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
diabetes, psoriasis and glaucoma.

XX Claim 20; Page -; 158pp; English.

XX The invention describes novel nucleic acids encoding Interleukin (IL) 17  
receptor like polypeptides useful as vaccines and in gene therapy. These  
have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
ophthalmological activities. The IL-17 receptor like nucleic acids and  
proteins may be used to prevent and treat diseases associated with  
inappropriate IL-17 receptor like polypeptide (IL17R) expression. These  
include, for example immune disorders (e.g. inflammation, diabetes and  
transplant rejection), infections (e.g. hepatitis and septicemia),  
weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
(e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
(e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
breast cancer), reproductive disorders (e.g. infertility and  
miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
DNA and its complements may also be used as diagnostic probes to detect and  
quantitate the presence of similar nucleic acids in samples and identify  
patients needing restorative therapy. The IL17R may also be used as  
antigens in the production of antibodies against the proteins and in

CC assays to identify modulators of expression and activity. The  
anti-IL17R antibodies and antagonists may also be used to down regulate  
expression and activity.  
CC Note: This sequence is not given in the specification but is based on the  
human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
and has been created according to information given in claim 20.

XX Sequence 738 AA:

Query Match 97.1%; Score 3897; DB 22; Length 738;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;  
QY 1 MAPWLQCSVFFTVNACLSQSLAAAGGSGRARGADTCGRWKAARPRLCVANEVGP 60  
DB 1 MAPWLQCSVFFTVNACLSQSLAAAGGSGRARGADTCGRWKAARPRLCVANEVGP 60  
QY 61 ASRNSGLNITFKYDNCITTYLNPVGHVIAADQNITISQYACHQDVAVTILWSPGALGIE 120  
DB 47 ASRNSGLNITFKYDNCITTYLNPVGHVIAADQNITISQYACHQDVAVTILWSPGALGIE 106  
QY 121 FLKGRFVILEELKSGRQCCQLILKDPQLNSFKRTGMSQFPLMKPFTDYFKVVPF 180  
DB 107 FLKGRFVILEELKSGRQCCQLILKDPQLNSFKRTGMSQFPLMKPFTDYFKVVPF 166  
QY 181 PSIKNESNTHPFFTRACDILLQPDNLACKPFWKPNLNISQHSQSDMOVSFDHAPNFG 240  
DB 167 PSIKNESNTHPFFTRACDILLQPDNLACKPFWKPNLNISQHSQSDMOVSFDHAPNFG 226  
QY 241 PRFYLYHLKHGEPFKRTKQEQTTTSCLLQNVSPGDIILVDDTNTTRKVMHYA 300  
DB 227 PRFYLYHLKHGEPFKRTKQEQTTTSCLLQNVSPGDIILVDDTNTTRKVMHYA 286  
QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRRKQOENIYSHLDESSESTYTA 360  
DB 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCRRKQOENIYSHLDESSESTYTA 346  
QY 361 LPRLRPRPKVPLCYSSKQGNHNVVOCFAFLQDFCGCEVALDLWDFSLCREGORE 420  
DB 347 LPRLRPRPKVPLCYSSKQGNHNVVOCFAFLQDFCGCEVALDLWDFSLCREGORE 406  
QY 421 WVIOKIHESOFITVCSKGMKYFYDKKNYKHGGGSGSGELFVAVSAIAELRQAKQ 480  
DB 407 WVIOKIHESOFITVCSKGMKYFYDKKNYKHGGGSGSGELFVAVSAIAELRQAKQ 466  
QY 481 SSSAALSKEFLAVFYDSCGDPVGLDLSYKRLMDNLPCLSHLSRDRGLQERQHTR 540  
DB 467 SSSAALSKEFLAVFYDSCGDPVGLDLSYKRLMDNLPCLSHLSRDRGLQERQHTR 526  
QY 541 QGSRNTRFSKSGRSIYVAICNMHOFIDEEPDMFEKQFVFPFPPPLRYREPVLKFDGSL 600  
DB 527 QGSRNTRFSKSGRSIYVAICNMHOFIDEEPDMFEKQFVFPFPPPLRYREPVLKFDGSL 586  
QY 601 VLNDVCKPESDFCLKVEAAVLGATGPADQSQHSQHGGLDQDGEARPDGSAALQPL 660  
DB 587 VLNDVCKPESDFCLKVEAAVLGATGPADQSQHSQHGGLDQDGEARPDGSAALQPL 646  
QY 661 LHTVKGSPDMPRDSGIYDSSVPSSELSPLMEGLSTDTTSSLTSSYSSSSSGLGEE 720  
DB 647 LHTVKGSPDMPRDSGIYDSSVPSSELSPLMEGLSTDTTSSLTSSYSSSSSGLGEE 706  
QY 721 PPALPSKLLSSGCKADLCGRSYTDELHAVAP 752  
DB 707 PPALPSKLLSSGCKADLCGRSYTDELHAVAP 738

## RESULT 6

AAU09954

ID AAU09954 standard; Protein: 738 AA

XX AC AAU09954;

XX 14-FEB-2002 (first entry)



KW mulein.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 45  
 FT /label= Gly, Pro or Ala  
 XX  
 PN WO200168859-A2  
 XX  
 PD 20-SEP-2001  
 XX  
 PF 15-MAR-2001; 2001NO-US08678.  
 XX  
 PR 16-MAR-2000; 2000US-189816P.  
 XX  
 PR 28-NOV-2000; 2000US-0724460.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Jing S;  
 XX  
 DR WPI: 2001-611392/70.  
 XX

Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 diabetes, psoriasis and glaucoma

Claim 18; Page -; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17  
 receptor like polypeptides useful as vaccines and in gene therapy. These  
 have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and  
 ophthalmological activities. The IL-17 receptor like nucleic acids and  
 proteins may be used to prevent and treat diseases associated with  
 inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These  
 include, for example immune disorders (e.g. inflammation, diabetes and  
 transplant rejection), infections (e.g. hepatitis and septicaemia),  
 weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 breast cancer), reproductive disorders (e.g. infertility and  
 miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 DNA and its complements may also be used as diagnostic probes to detect and  
 patients needing restorative therapy. The IL17rp may also be used as  
 antigens in the production of antibodies against the proteins and in  
 assays to identify modulators of expression and activity. The  
 anti-IL17rp antibodies and antagonists may also be used to down regulate  
 expression and activity.

Note: This sequence is not given in the specification but is based on the  
 human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 and has been created according to information given in claim 18.

Sequence 738 AA;

Query Match 97.0%; Score 3894; DB 22; Length 738;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPHLQCSVEFTVNAACLSQAVAGSGRGACATCGRMKAARPLCVANEGVGP 60  
 DB 1 MAPHLQCSVEFTVNAACLSQAVAGSGRGACATCGRMKAARPLCVANEGVGP 46  
 QY 61 ASRNSGLNYITFYDNCITVLPVGVKHVIADANITISQYACHQDVAVTILMSPGALGIE 120  
 DB 47 ASRNSGLNYITFYDNCITVLPVGVKHVIADANITISQYACHQDVAVTILMSPGALGIE 106

QY 121 FLKGFVILLEKSGROCOOLILKDPKQLNSSFKRTGMSOPFLNMKFETDYFKVVPF 180  
 DB 107 FLKGFVILLEKSGROCOOLILKDPKQLNSSFKRTGMSOPFLNMKFETDYFKVVPF 166  
 QY 181 PSIKNESNTHPFFTRACDLLLLQPDNLACKPFWKPRNLNLSHQSGDMQVDFHAPNFG 240  
 DB 167 PSIKNESNTHPFFTRACDLLLLQPDNLACKPFWKPRNLNLSHQSGDMQVDFHAPNFG 226  
 QY 241 FRFFYLHYLKLHEGPFKRTCKQBOFTTETTSCLLQNVSPGDYIELVDOTNTRKVMHYA 300  
 DB 227 FRFFYLHYLKLHEGPFKRTCKQBOFTTETTSCLLQNVSPGDYIELVDOTNTRKVMHYA 286  
 QY 301 LKPVHSPWAGPTRAIVATVPLVWISAFATLFTVWCKRKQENIYSHLDEESESSTYTA 360  
 DB 287 LKPVHSPWAGPTRAIVATVPLVWISAFATLFTVWCKRKQENIYSHLDEESESSTYTA 346  
 QY 361 LPRERLRPRKVFVLCYSSKQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420  
 DB 347 LPRERLRPRKVFVLCYSSKQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 406  
 QY 421 WVIQKHESQFIIVYCSKGMKVFYDKKNTYKRGSGRGKGEFLVAVSAEKLRAQK 480  
 DB 407 WVIQKHESQFIIVYCSKGMKVFYDKKNTYKRGSGRGKGEFLVAVSAEKLRAQK 466  
 QY 481 SSSAALSKEFIAYFYDSCGDPVGLDLSKYRLMDNLPLCLSHLSHRDHGLQEPGQHT 540  
 DB 467 SSSAALSKEFIAYFYDSCGDPVGLDLSKYRLMDNLPLCLSHLSHRDHGLQEPGQHT 526  
 QY 541 QGSRNRYFKSGRSLSYVAICNMHOFIDEPDMFEKQFVFPFPPPLRYREPVLKFDSDGL 600  
 DB 527 QGSRNRYFKSGRSLSYVAICNMHOFIDEPDMFEKQFVFPFPPPLRYREPVLKFDSDGL 586  
 QY 601 VLNDVCKGPESDCLVKEAVATGATGADSDSHQSHOGGLDQDGEARPALDGGSAALOPL 660  
 DB 587 VLNDVCKGPESDCLVKEAVATGATGADSDSHQSHOGGLDQDGEARPALDGGSAALOPL 646  
 QY 661 LHTVKAGSDMPROSGIYDSSVPSSELSPLMEGLSTDTQTETSSLTSSVSSSGSGAGEE 720  
 DB 647 LHTVKAGSDMPROSGIYDSSVPSSELSPLMEGLSTDTQTETSSLTSSVSSSGSGAGEE 706  
 QY 721 PPALPSKLLSSGSCRADLGCSTYDELHAYAP 752  
 DB 707 PPALPSKLLSSGSCRADLGCSTYDELHAYAP 738

RESULT 8  
 AAU09952  
 ID AAU09952 standard; Protein; 738 AA.  
 XX  
 AC AAU09952;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #2.  
 XX  
 KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW mulein.  
 KW Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 227  
 FT /label= Phe, Leu, Val, Ile, Ala, Tyr  
 XX  
 FT WO200168859-A2.  
 PN



XX PD 20-SEP-2001.  
 XX PF 15-MAR-2001; 2001WO-US08678.  
 XX PR 16-MAR-2000; 2000US-189816P.  
 XX PR 28-NOV-2000; 2000US-0724460.  
 XX PA (AMGE-) AMGEN INC.  
 XX PI Jing S;  
 XX DR WPI; 2001-611392/70.  
 XX FT Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 XX FT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 XX FT diabetes, psoriasis and glaucoma.  
 XX PS Claim 19; Page.: 158pp; English.  
 XX CC The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 CC osteopathic, vascular, cytosolic, anti-leukemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17r) expression. These  
 CC include, for example, immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17r may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17r antibodies and antagonists may also be used to down regulate  
 CC expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AA009904)  
 CC and has been created according to information given in claim 19.  
 XX SQ Sequence 738 AA;  
 Query Match 97.0%; Score 3894; DB 22; Length 738;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;  
 QY 1 MAPWLQCSVFETYNACLSQAVAGSGRGARGADTCGRMRMAAPRLCVANGVGP 60  
 DB 1 MAPWLQCSVFETYNACLSQAVAGSGRGARGADTCGRMRMAAPRLCVANGVGP 60  
 QY 61 ASRNSGLYNITFKYDNCNTTLYNPVGRKVIADQAQNTISQYACHDQVAVTILWSPGALGIE 120  
 DB 47 ASRNSGLYNITFKYDNCNTTLYNPVGRKVIADQAQNTISQYACHDQVAVTILWSPGALGIE 106  
 QY 121 FLKGRFVILELSEKSGCCQLIKDPKOLNSFKETGCHESQPLNKKFTDYFKVVPF 180  
 DB 107 FLKGRFVILELSEKSGCCQLIKDPKOLNSFKETGCHESQPLNKKFTDYFKVVPF 166  
 QY 181 PSIKNESYHFFFTFRACDLLOPDLACKPFWKPRNLNLSQHGSDMQVSEFDHAPNFG 240  
 DB 167 PSIKNESYHFFFTFRACDLLOPDLACKPFWKPRNLNLSQHGSDMQVSEFDHAPNFG 226  
 QY 241 FRFFLYLHYKLKHEGPFKRKCKQBQTTTSCLLQNVSPGDYIIELVDDTNTTKVHYA 300

DB 227 XRFYLYLHYKLKHEGPFKRKCKQBQTTTSCLLQNVSPGDYIIELVDDTNTTKVHYA 286  
 QY 301 LKPVHSPWAGPIRAVATVPLVVISAFATLFTVCKRKQENIYSHLDRESSSSTYTA 360  
 DB 287 LKPVHSPWAGPIRAVATVPLVVISAFATLFTVCKRKQENIYSHLDRESSSSTYTA 346  
 QY 361 LPRERLRPRPKVFLCYSSKDGQNHNVVQCFAIFLQDFCGCEVALDLDWEDFSLCREGORE 420  
 DB 347 LPRERLRPRPKVFLCYSSKDGQNHNVVQCFAIFLQDFCGCEVALDLDWEDFSLCREGORE 406  
 QY 421 WYIQIHEHQPIIYVCSKGMKYFVDKKNYKKGGRGSGKGEFLVAVSAIAEKLROAKO 480  
 DB 407 WYIQIHEHQPIIYVCSKGMKYFVDKKNYKKGGRGSGKGEFLVAVSAIAEKLROAKO 466  
 QY 481 SSSAALSXFIAYVYDYSCEGDVPGIILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPQHTR 540  
 DB 467 SSSAALSXFIAYVYDYSCEGDVPGIILDLSTKYRLMDNLPQLCSHLHSRDHGLQEPQHTR 526  
 QY 541 QGSRNRYFRSGRSRLYVAICNNHQFIDEEPWFKEQFVPPHPPPLRYREPVLKFDSDL 600  
 DB 527 QGSRNRYFRSGRSRLYVAICNNHQFIDEEPWFKEQFVPPHPPPLRYREPVLKFDSDL 586  
 QY 601 VLNDVCKRGPESDFCLKVEAVLGNATGPADSOHESQHGGLDQGEARPALDGSAAALQPL 660  
 DB 587 VLNDVCKRGPESDFCLKVEAVLGNATGPADSOHESQHGGLDQGEARPALDGSAAALQPL 646  
 QY 661 LHTVAGSPDMPDRDSDIYDSSVPSSELSLPLMEGLSTDTQTSTSSVSSSSGLGEE 720  
 DB 647 LHTVAGSPDMPDRDSDIYDSSVPSSELSLPLMEGLSTDTQTSTSSVSSSSGLGEE 706  
 QY 721 PPALPSKLLSGSGCKADLCGRSYTDELHAVAP 752  
 DB 707 PPALPSKLLSGSGCKADLCGRSYTDELHAVAP 738  
 RESULT 9  
 AA009956  
 ID AA009956 standard; Protein; 738 AA.  
 XX AC AA009956;  
 XX DT 14-FEB-2002 (first entry)  
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #6.  
 KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytosolic; anti-leukemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW muteln.  
 XX KW Homo sapiens.  
 OS Synthetic.  
 XX FT Key Location/Qualifiers  
 FT Misc-difference 515 /label= Asp, Glu  
 XX WO200168859-A2.  
 XX PD 20-SEP-2001.  
 XX PF 15-MAR-2001; 2001WO-US08678.  
 XX PR 16-MAR-2000; 2000US-189816P.  
 XX PR 28-NOV-2000; 2000US-0724460.  
 XX PA (AMGE-) AMGEN INC.



PI XJing S;  
 DR WPI: 2001-611392/70.  
 XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,  
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 PT diabetes, psoriasis and glaucoma.  
 XX Claim 23; Page 1; 158pp; English.  
 XX The invention describes novel nucleic acids encoding Interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-asthmatic, dermatological,  
 CC anti-parkinsonian, anti-convulsant, anti-leukemic, anti-infertility and  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantify the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17rp may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17rp antibodies and antagonists may also be used to down regulate  
 CC expression and activity.  
 CC Note: This sequence is not given in the specification but is based on the  
 CC human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 CC and has been created according to information given in claim 23.

XX Sequence 738 AA;  
 SQ

Query Match 97.0%; Score 3894; DB 22; Length 738;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPWLQCSVFFTVNACLSQSLAAGSGRAGADTCGRKAAARPLCVANEGVCP 60  
 DB 1 MAPWLQCSVFFTVNACLSQSLAAGSGRANGVTCGR-----GVGP 46  
 QY 61 ASRNSGLNITFYKDYNTLNPVKHVIADQNITISQYACHQVAVTILSPGALGIE 120  
 DB 47 ASRNSGLNITFYKDYNTLNPVKHVIADQNITISQYACHQVAVTILSPGALGIE 106  
 QY 121 FLKGFVILELASEGRCQQLILDKPKLNSFFRTGMSQPFPLNKKETDYFKVVPF 180  
 DB 107 FLKGFVILELASEGRCQQLILDKPKLNSFFRTGMSQPFPLNKKETDYFKVVPF 166  
 QY 181 PSIKNESNYHFFFRFACDLLOPNLACRFKPKRNLTISQHSQDMQVSDHAPHNFG 240  
 DB 167 PSIKNESNYHFFFRFACDLLOPNLACRFKPKRNLTISQHSQDMQVSDHAPHNFG 226  
 QY 241 FRFFLYHKLKHBGPKFKTKQEQOTTETTSCLLNQVSPGDYIELVDNTTRKVMHYA 300  
 DB 227 FRFFLYHKLKHBGPKFKTKQEQOTTETTSCLLNQVSPGDYIELVDNTTRKVMHYA 286  
 QY 301 LKPVHSPWAGPIRAVAITPLVVISAFATLFTVWCKRKQENIYSHLDESSSTYTA 360  
 DB 287 LKPVHSPWAGPIRAVAITPLVVISAFATLFTVWCKRKQENIYSHLDESSSTYTA 346  
 QY 361 LPRERLRPRKVFCLTSSKDGQNHNNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420  
 DB 347 LPRERLRPRKVFCLTSSKDGQNHNNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 406

OY 421 WVIQKTHESOFIIVCWSKGMKYFVDKKNYKHGGSGRGKGLFVLVAVSAIAEKLRQAKQ 480  
 DB 407 WVIQKTHESOFIIVCWSKGMKYFVDKKNYKHGGSGRGKGLFVLVAVSAIAEKLRQAKQ 466  
 OY 481 SSSAALSKEFTAVFYDYSCEGDVPGILDISTKYRLMDNLPCLSHLHSRDRHGLQEPGQHR 540  
 DB 467 SSSAALSKEFTAVFYDYSCEGDVPGILDISTKYRLMDNLPCLSHLHSRDRHGLQEPGQHR 526  
 OY 541 QGSRNRYFRSKSGRSYVAICNMHOFIDEEPDPWEKOFVFPHPPLRYREPVEKFDGSL 600  
 DB 527 QGSRNRYFRSKSGRSYVAICNMHOFIDEEPDPWEKOFVFPHPPLRYREPVEKFDGSL 586  
 OY 601 VLNDVMCKPGPESDFCLKVEAVYLGATGPADQSQHSQHGGLDQDGEARPALDGSAAQPL 660  
 DB 587 VLNDVMCKPGPESDFCLKVEAVYLGATGPADQSQHSQHGGLDQDGEARPALDGSAAQPL 646  
 OY 661 LHTVKAGSPDMPRDSGIYDSSVSPSELSPMBGLSTDTQETSSITSSVSSSSGLGEE 720  
 DB 647 LHTVKAGSPDMPRDSGIYDSSVSPSELSPMBGLSTDTQETSSITSSVSSSSGLGEE 706  
 OY 721 PPALPSKLLSSGCKADLCRSYTDHVAAP 752  
 DB 707 PPALPSKLLSSGCKADLCRSYTDHVAAP 738  
 RESULT 10  
 AAU09955  
 ID AAU09955 standard; Protein; 738 AA.  
 AC AAU09955;  
 XX 14-FEB-2002 (first entry)  
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #5.  
 KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW muteln.  
 XX Homo sapiens.  
 QS Synthetic.  
 PH Key Location/Qualifiers  
 FT Misc-difference 385 /label- Cys, Ser, Ala  
 XX WO200168859-A2.  
 XX 20-SEP-2001.  
 XX 15-MAR-2001; 2001WO-US08678.  
 XX 16-MAR-2000; 2000US-189816P.  
 XX 28-NOV-2000; 2000US-0724460.  
 XX (AMGE-) AMGEN INC.  
 XX Jing S;  
 XX WPI: 2001-611392/70.  
 XX Nucleic acids encoding Interleukin 17 receptor like polypeptides,  
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 PT diabetes, psoriasis and glaucoma.  
 XX Claim 22; Page 1; 158pp; English.  
 XX

CC The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17r) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and  
 CC transplant rejection), infections (e.g. hepatitis and septicemia),  
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 CC bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders  
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and  
 CC breast cancer), reproductive disorders (e.g. infertility and  
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 CC DNA and its complements may also be used as diagnostic probes to detect and  
 CC quantitate the presence of similar nucleic acids in samples and identify  
 CC patients needing restorative therapy. The IL17r may also be used as  
 CC antigens in the production of antibodies against the proteins and in  
 CC assays to identify modulators of expression and activity. The  
 CC anti-IL17r antibodies and antagonists may also be used to down regulate  
 CC expression and activity.  
 CC Note: this sequence is not given in the specification but is based on the  
 CC human interleukin 17 (IL-17) receptor like protein sequence (AAU09904)  
 CC and has been created according to information given in claim 22.

XX Sequence : 738 AA;

Query Match 96.9%; Score 3890; DB 22; Length 738;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPWQLQSVFTNACLSQAVAGSGRGARGADTCGRMKAAARPRCLVANEGVGP 60  
 DB 1 MAPWQLQSVFTNACLSQAVAGSGRGARGADTCGRMKAAARPRCLVANEGVGP 60  
 QY 61 ASRNSGLNITFKYDNCNTTILNPKGVKHTADANITISQYACHQVAVTILWSPGALGIE 120  
 DB 47 ASRNSGLNITFKYDNCNTTILNPKGVKHTADANITISQYACHQVAVTILWSPGALGIE 106  
 QY 121 FLKGRVILEELKSEGRCQOLIKDPKOLNSFKRTGNSQPELNMKFFEDYFKVVPF 180  
 DB 107 FLKGRVILEELKSEGRCQOLIKDPKOLNSFKRTGNSQPELNMKFFEDYFKVVPF 166  
 QY 181 PSIKESNYHPPFTRACDILLOPDLACKPFWKPRNLISQHSQDMQVSDHAPNFG 240  
 DB 167 PSIKESNYHPPFTRACDILLOPDLACKPFWKPRNLISQHSQDMQVSDHAPNFG 226  
 QY 241 FRFFYLHYKLHKGEPFKRTCKOBTETTSCLLQNVSPGYIIELVDDNTTKVNVYA 300  
 DB 227 FRFFYLHYKLHKGEPFKRTCKOBTETTSCLLQNVSPGYIIELVDDNTTKVNVYA 286  
 QY 301 LKPVISWAGIRAVATVPLVWISAFATLVNCRKKQENIYSHLDESSSSTYTA 360  
 DB 287 LKPVISWAGIRAVATVPLVWISAFATLVNCRKKQENIYSHLDESSSSTYTA 346  
 QY 361 LPRRLRPRPVFLCYSSKQGNHNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420  
 DB 347 LPRRLRPRPVFLCYSSKQGNHNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 406  
 QY 421 WYQKHESQIIVVCYSGKMYFVDKNTKHGGGSGKGLFLVAVSAIAELKRAQK 480  
 DB 407 WYQKHESQIIVVCYSGKMYFVDKNTKHGGGSGKGLFLVAVSAIAELKRAQK 466  
 QY 481 SSSAALSFIAYFDYCEGDVPGILDSTKYRLMDNLPQLCSHLHSDRGHLEPQOHR 540  
 DB 467 SSSAALSFIAYFDYCEGDVPGILDSTKYRLMDNLPQLCSHLHSDRGHLEPQOHR 526  
 QY 541 QCSRNYFRSGSLYVAICNHNQFIDEPDFEKFQVPPHPPPLRYRPPVLEKFDGSL 600

DB 527 QCSRNYFRSGSLYVAICNHNQFIDEPDFEKFQVPPHPPPLRYRPPVLEKFDGSL 586  
 QY 601 VLNDVCKPGPESDFCLKYBAVVLGATGPADSOHESORGGGLDQGEAPALDGSAAQPL 660  
 DB 587 VLNDVCKPGPESDFCLKYBAVVLGATGPADSOHESORGGGLDQGEAPALDGSAAQPL 646  
 QY 661 LHTVAGSPDMPRDGIYDSSVSPSELSLPLMEGLSTDQTFSTSTESVSSSGIGREE 720  
 DB 647 LHTVAGSPDMPRDGIYDSSVSPSELSLPLMEGLSTDQTFSTSTESVSSSGIGREE 706  
 QY 721 PPALPSKLLSGSGCKADLCGRSYTDELHAPV 752  
 DB 707 PPALPSKLLSGSGCKADLCGRSYTDELHAPV 738

# RESULT 11

AAU09957 standard; Protein; 738 AA.

XX AAU09957;

XX 14-FEB-2002 (first entry)

XX Human Interleukin 17 (hIL-17) receptor like protein substitution #7.

XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;  
 KW mutin.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 602

XX /label= Cys, Ala, Ser

XX WO200168859-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-US08678.

XX 16-MAR-2000; 2000US-189816P.

XX 28-NOV-2000; 2000US-0724460.

XX (AMGE-) AMGEN INC.

XX Jing S;

XX WPI; 2001-611392/70.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 PT useful for preventing, diagnosing and treating, e.g. leukemia, asthma,  
 PT diabetes, psoriasis and glaucoma.

XX Claim 24; Page : 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 CC receptor like polypeptides useful as vaccines and in gene therapy. These  
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and  
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and  
 CC proteins may be used to prevent and treat diseases associated with  
 CC inappropriate IL-17 receptor like polypeptide (IL17r) expression. These  
 CC include, for example immune disorders (e.g. inflammation, diabetes and

transplant rejection), infections (e.g. hepatitis and septicaemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity.

Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 24.

XX Sequence 738 AA;

Query Match 96.9%; Score 3890; DB 22; Length 738;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPMLQLCSVFFTVNACLSGSLAVALAAGSGRAGADTCGRKAAARPLCVANEGVGP 60  
DB 1 MAPMLQLCSVFFTVNACLSGSLAVALAAGSGRANGVDTGGR-----GVGP 46

QY 61 ASRNSGLNITFKYDNTCTYLPVGVKHVIADAQNTISQYACHQVAVYILMSPGALGIE 120  
DB 47 ASRNSGLNITFKYDNTCTYLPVGVKHVIADAQNTISQYACHQVAVYILMSPGALGIE 106

QY 121 FLKGFVILBELSEGRQCCQLILADPKQLNSFKRTGMSQPPFNKKEFTDYFKVYVFF 180  
DB 107 FLKGFVILBELSEGRQCCQLILADPKQLNSFKRTGMSQPPFNKKEFTDYFKVYVFF 166

QY 181 PSIKNESNYHPPFRFRACDILLDPNLACKPFKPRNLNLSQSGDMOVSDHAPHNG 240  
DB 167 PSIKNESNYHPPFRFRACDILLDPNLACKPFKPRNLNLSQSGDMOVSDHAPHNG 226

QY 241 FRFFLYKLKHEGPFKRTCKQQTETTSCLLQNSPGDYIELVDQNTTRKVMYA 300  
DB 227 FRFFLYKLKHEGPFKRTCKQQTETTSCLLQNSPGDYIELVDQNTTRKVMYA 286

QY 301 LKPVHSPWAGPIRAVATVPLVVISAFATLFTVCKKQENIYSHLDESSSESTYAA 360  
DB 287 LKPVHSPWAGPIRAMAITVPLVVISAFATLFTVCKKQENIYSHLDESSSESTYAA 346

QY 361 LPRELPRPKVFLCYSSKQGNHNVVQCFAYFLQDFCCEVALQWEDFSLCREGORE 420  
DB 347 LPRELPRPKVFLCYSSKQGNHNVVQCFAYFLQDFCCEVALQWEDFSLCREGORE 406

QY 421 VWIKIHESEFIIVCSKGMKVFVKNNYKHGGGSGRGELFLVAVSAIAEKLRAQK 480  
DB 407 VWIKIHESEFIIVCSKGMKVFVKNNYKHGGGSGRGELFLVAVSAIAEKLRAQK 466

QY 481 SSSAALSKEFNAVFDYSCGDPVGLDILSTYKRLMDNLPOLCSHLHSRQHGLOEPQHT 540  
DB 467 SSSAALSKEFNAVFDYSCGDPVGLDILSTYKRLMDNLPOLCSHLHSRQHGLOEPQHT 526

QY 541 QCSRRTFRSKGRSLYVAICNNHQFIDEEPWFKEKQVFPFPPPLRYREPVLKFDGL 600  
DB 527 QCSRRTFRSKGRSLYVAICNNHQFIDEEPWFKEKQVFPFPPPLRYREPVLKFDGL 586

QY 601 VLVNDVCKPGPESDPCLVKEAVVILGATGPADSOHESQHGGLDQGGARPALDGSALQPL 660  
DB 587 VLVNDVCKPGPESDPCLVKEAVVILGATGPADSOHESQHGGLDQGGARPALDGSALQPL 646

QY 661 LHTVAGSPDMFRDGIYDSSVPSSELSLPLMEGLSTDDTETSSLTESVSSSSGLGEE 720  
DB 647 LHTVAGSPDMFRDGIYDSSVPSSELSLPLMEGLSTDDTETSSLTESVSSSSGLGEE 706

QY 721 PPALPSKLLSSGCKADLCGRSYTDELHAVAP 752  
DB 707 PPALPSKLLSSGCKADLCGRSYTDELHAVAP 738

## RESULT 12

AAU11355  
ID AAU11355 standard; Protein: 738 AA.

XX AC AAU11355;

XX 26-MAR-2002 (first entry)

XX Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide.

XX Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling;  
KW gene therapy; protein therapy; immunological disorder.

XX Homo sapiens.

XX Key: Location/Qualifiers

XX Misc-difference 25

XX /label= Val

XX /note= "Encoded by GTN"

XX WO200190358-A2.

XX 29-NOV-2001.

XX 23-MAY-2001; 2001WO-US16767.

XX 24-MAY-2000; 2000US-206862P.

XX (SCHE ) SCHERING CORP.

XX Gorman DN;

XX WPI; 2002-106198/14.

XX N-PSDB; AAS18134.

XX Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide useful for detecting antibodies generated in response to presence of increased protein levels or immunological disorders -

XX Claim 1; Page 25; 148pp; English.

XX The invention relates to primate and rodent DNAX cytokine receptor subunit (DCRS) polypeptides and the polynucleotides encoding them. The receptors, or their portions may be useful as phosphate labelling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognising antibodies, or antigens capable of binding antibodies. A combination, e.g., including a DCRS can be used as an immunogen for the production of antisera or antibodies capable of distinguishing between other cytokine receptor family members. A purified DCRS can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. This sequence represents the human DCRS8 polypeptide.

XX Sequence 738 AA;

Query Match 95.5%; Score 3830.5; DB 23; Length 738;

Best Local Similarity 96.3%; Pred. No. 0;

Matches 725; Conservative 2; Mismatches 11; Indels 15; Gaps 2;

QY 1 MAPMLQLCSVFFTVNACLSGSLAVALAAGSGRAGADTCGRKAAARPLCVANEGVGP 60

DB 1 MAPMLQLCSVFFTVNACLSGSLAVALAAGSGRAGADTCGRKAAARPLCVANEGVGP 46

QY 61 ASRNSGLNITFKYDNTCTYLPVGVKHVIADAQNTISQYACHQVAVYILMSPGALGIE 120

Db 47 ASRNSGLNITFKYDNCITLNPVKHVIADQNIITISQACHQVAVTILMSFALGIE 106  
 QY 121 FLKGFVILIELKSGRQCOQLILKDPKQNSFKRTGMSOPFLNMFETDYFVKVPF 180  
 Db 107 FLKGFVILIELKSGRQCOQLILKDPKQNSFKRTGMSOPFLNMFETDYFVR-LSF 165  
 QY 181 PSKNSNTHPFFETFRACDILLOPDNLACKPFWKPRNLNISORGSQMOVSFDPHAPNFG 240  
 Db 166 SFKNSNTHPFFETFRACDILLOPDNLACKPFWKPRNLNISORGSQMOVSFDPHAPNFG 225  
 QY 241 FRFYLHYLKHGPKRTCKQBTFTTSCLLQNVSPGDIILVDDTNTTKRVHYA 300  
 Db 226 FRFYLHYLKHGPKRTCKQBTFTTSCLLQNVSPGDIILVDDTNTTKRVHYA 285  
 QY 301 LKPVHSPAGPIRAVAITVPLVISAFAITLVNCRKQKQNIYSHLDEESSESTYTA 360  
 Db 286 LKPVHSPAGPIRAVAITVPLVISAFAITLVNCRKQKQNIYSHLDEESSESTYTA 345  
 QY 361 LPRERLRPRKPVFLCYSSKQNGHNVVQCFAYFLQDFCGCEVALDLMEDFSLCREGORE 420  
 Db 346 LPRERLRPRKPVFLCYSSKQNGHNVVQCFAYFLQDFCGCEVALDLMEDFSLCREGORE 405  
 QY 421 WYOKTHESQFIIVVCSKGMFYVDKNYKHGGRSGKGBELFVAVSAIAEKLRQAKQ 480  
 Db 406 WYOKTHESQFIIVVCSKGMFYVDKNYKHGGRSGKGBELFVAVSAIAEKLRQAKQ 465  
 QY 481 SSSAALSKEFIATVFDYSCGDPVGLDLSLTKYRLMDNLPLQCLSHLSRDHGLQBPQGHTR 540  
 Db 466 SSSAALSKEFIATVFDYSCGDPVGLDLSLTKYRLMDNLPLQCLSHLSRDHGLQBPQGHTR 525  
 QY 541 QGSRRTYFKSGRSLYVAICNMHOFIDBPDPFKEQFVFPFPPPLRYREPVLEKFSGL 600  
 Db 526 QGSRRTYFKSGRSLYVAICNMHOFIDBPDPFKEQFVFPFPPPLRYREPVLEKFSGL 585  
 QY 601 VLNDVCKPGPESDCLAVEAALVGTGTPADSDQHSQHGLDQDCEARPALDGSAAQLPL 660  
 Db 586 VLNDVCKPGPESDCLAVEAALVGTGTPADSDQHSQHGLDQDCEARPALDGSAAQLPL 645  
 QY 661 LHTVAGSPDMPROSGIYDSVSSLSPLMEGLSTQDTSTSLTESVSSSGLGEE 720  
 Db 646 LHTVAGSPDMPROSGIYDSVSSLSPLMEGLSTQDTSTSLTESVSSSGLGEE 705  
 QY 721 PPALPSKLLSSGCRADIGCRSYDELHVAAPL 733  
 Db 706 PPALPSKLLSSGCRADIGCRSYDELHVAAPL 738

RESULT 13  
 AAU04958  
 ID AAU04958 standard; Protein: 728 AA.  
 XX  
 AC AAU04958;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human Interleukin 17 receptor, IL-17RH4.  
 XX  
 KW Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist;  
 KW rheumatoid arthritis; DNA 154095-2998; systemic lupus erythematosus;  
 KW allergic disease; asthma; demyelinating disease;  
 KW degenerative cartilaginous disorder; transplantation associated disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT Region 19..24 "N-myristoylation site"  
 FT Modified-site 31..34 "Asn is N-glycosylated"  
 FT Modified-site 38..41 "Asn is N-glycosylated"  
 FT Modified-site 56..59 "Asn is N-glycosylated"

FT Modified-site 113..116 /note- "Asn is N-glycosylated"  
 FT Modified-site 147..150 /note- "Asn is N-glycosylated"  
 FT Modified-site 182..185 /note- "Asn is N-glycosylated"  
 FT Region 232..235 /note- "Asn is N-glycosylated"  
 FT Phosphorylation site 266..269 /note- "cAMP/GMP-dependent protein kinase phosphorylation site"  
 FT Domain 283..307 /note- "Asn is N-glycosylated"  
 FT Region 312..319 /note- "Transmembrane domain"  
 FT Region 375..380 /note- "Tyrosine kinase phosphorylation site"  
 FT Region 416..424 /note- "N-myristoylation site"  
 FT Region 428..433 /note- "Tyrosine kinase phosphorylation site"  
 FT Region 429..434 /note- "N-myristoylation site"  
 FT Region 432..437 /note- "N-myristoylation site"  
 FT Region 433..436 /note- "N-myristoylation site"  
 FT Region 517..522 /note- "Glycosaminoglycan attachment site"  
 FT Region 574..579 /note- "N-myristoylation site"  
 FT Region 652..657 /note- "N-myristoylation site"  
 FT Region 707..712 /note- "N-myristoylation site"  
 FT /note- "N-myristoylation site"  
 XX WO200146420-A2.  
 XX  
 PD 28-JUN-2001.  
 XX  
 PF 20-DEC-2000; 2000WO-US34956.  
 XX  
 PR 23-DEC-1999; 99US-0172096.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 11-JAN-2000; 2000US-0175481.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 21-MAR-2000; 2000US-0191007.  
 PR 02-JUN-2000; 2000WO-US07532.  
 PR 22-JUN-2000; 2000US-0213087.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-OCT-2000; 2000WO-US23328.  
 PR 24-OCT-2000; 2000US-0242837.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 28-NOV-2000; 2000US-0253646.  
 PR 01-DEC-2000; 2000WO-US32678.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;  
 PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL;  
 PI Watanabe CK, Williams PM, Wood WI, Yansura DG;  
 XX  
 DR WPI; 2001-451708/48.  
 DR N-PSDB; AAS09517.  
 XX  
 PT Novel PRO polypeptides homologous to interleukin-17, useful for the  
 PT diagnosis and treatment of immune related disease e.g. rheumatoid  
 PT arthritis and diabetes.  
 XX  
 PS Claim 10; Fig 18; 188pp; English.

XX The sequence is PRO20026 which is the human Interleukin 17 receptor,  
 CC IL-17RA, encoded by DNA 154095-2998. A composition  
 CC containing anti/agonists to the PRO polypeptides or individual components  
 CC are useful for treating a mammal with an immune related disease, e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, a demyelinating disease, an autoimmune or immune-mediated skin  
 CC disease, contact dermatitis, an allergic disease e.g. food  
 CC hypersensitivity, asthma, a transplantation associated disease, or a  
 CC chronic inflammatory demyelinating polyneuropathy. Treating a  
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or  
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous  
 CC examples of the diseases and disorders are given in the specification.  
 XX SQ Sequence 728 AA;

Query Match 92.3%; Score 3703; DB 22; Length 728;  
 Best Local Similarity 96.7%; Pred. No. 0;  
 Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RKMAARPLCVAKE-GVGPASRNSGLYNITFKYDNCNTTYLNPVGRHVIADAGNITISY 100  
 Db 3 RASAGVPALEFGVGGVGPASRNSGLYNITFKYDNCNTTYLNPVGRHVIADAGNITISY 62  
 QY 101 ACHDOVAVTILWSPALGIEFLAGFRVILEELKSGRCQQLILKDPKQLNSFKRTGNE 160  
 Db 63 ACHDOVAVTILWSPALGIEFLAGFRVILEELKSGRCQQLILKDPKQLNSFKRTGNE 122  
 QY 161 SQPLFNKFFDYFKVVPVPPSKNESNTHPEFFRTRACDLLLQPNLACKPFWKPRNLN 220  
 Db 123 SQPLFNKFFDYFKVVPVPPSKNESNTHPEFFRTRACDLLLQPNLACKPFWKPRNLN 182  
 QY 221 ISQ-----HGSDQVSVFQHPHNFGRFFHYLYKHKHEGPKRKTCKEQBT 267  
 Db 183 ISQHGSDQVSVFQHPHNFGRFFHYLYKHKHEGPKRKTCKEQBT 242  
 QY 268 ETTSCLLQNVSPGDIIELVDDTNTTRKVMYALKPVHSPWAGPIRAVAITVPLVWISAF 327  
 Db 243 EMTSCLLQNVSPGDIIELVDDTNTTRKVMYALKPVHSPWAGPIRAVAITVPLVWISAF 302  
 QY 328 APLFTVMCKRQKQENIYSHLDESSSTYTAALPRERLRPRKVFICYSSKDGQNHNV 387  
 Db 303 APLFTVMCKRQKQENIYSHLDESSSTYTAALPRERLRPRKVFICYSSKDGQNHNV 362  
 QY 388 VOCFAYFLQDFCGCEVALDWEFSLCRREGQEWYQKHESQFIIVCSKGMKVFYDKK 447  
 Db 363 VOCFAIFLQDFCGCEVALDWEFSLCRREGQEWYQKHESQFIIVCSKGMKVFYDKK 422  
 QY 448 NYKHKGGRGSGKGFELVAVSAIAEKLQAKQSSAALSFKTAIVFYDSCGDVPGILD 507  
 Db 423 NYKHKGGRGSGKGFELVAVSAIAEKLQAKQSSAALSFKTAIVFYDSCGDVPGILD 482  
 QY 508 LSTKYRLMDNLPCLSHLSRDRHGLQEPQHTROGSRNTPRSKGRSLVATCNHOFI 567  
 Db 483 LSTKYRLMDNLPCLSHLSRDRHGLQEPQHTROGSRNTPRSKGRSLVATCNHOFI 542  
 QY 568 DEEPDWFKEQVPVPPHPPPLRYEPVLEKFDGLVNDVMCKPGPESDFCLKVEAAVLGAT 627  
 Db 543 DEEPDWFKEQVPVPPHPPPLRYEPVLEKFDGLVNDVMCKPGPESDFCLKVEAAVLGAT 602  
 QY 628 GPADSQSHSGHGLDQGEARPAIDGSAALQPLLTVKAGSPSPMDRSDGIYDSSVPSS 687  
 Db 603 GPADSQSHSGHGLDQGEARPAIDGSAALQPLLTVKAGSPSPMDRSDGIYDSSVPSS 662  
 QY 688 LSLPLMEGLSTDOTETSSLTSSVSSSGIGREEPPALPSKLLSGSGCKADLCGRSYTDEL 747  
 Db 663 LSLPLMEGLSTDOTETSSLTSSVSSSGIGREEPPALPSKLLSGSGCKADLCGRSYTDEL 722  
 QY 748 HAVAPL 753

Db 723 HAVAPL 728  
 RESULT 14  
 AAU10602  
 ID AAU10602 standard; Protein; 739 AA.  
 XX AAU10602;  
 AC AAU10602;  
 XX 14-FEB-2002 (first entry)  
 DT Human interleukin 17 (hIL-1) receptor-like protein version 2.  
 XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;  
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;  
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;  
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;  
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;  
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;  
 KW bone disease; vascular disorder; eye disorder; cancer; human.  
 XX Homo sapiens.  
 XX WO200168859-A2.  
 XX 20-SEP-2001.  
 XX 15-MAR-2001; 2001WO-US08678.  
 XX 16-MAR-2000; 2000US-189816P.  
 XX 28-NOV-2000; 2000US-0724460.  
 XX (AMGE-) AMGEN INC.  
 XX JIng S;  
 XX WPI: 2001-611392/70.  
 XX N-PSDB: AAS16201.  
 XX Nucleic acids encoding interleukin 17 receptor like polypeptides,  
 XX useful for preventing, diagnosing and treating, e.g. leukaemia, asthma,  
 XX diabetes, psoriasis and glaucoma.  
 XX Claim 2; Fig 1; 158pp: English.  
 XX The invention describes novel nucleic acids encoding interleukin (IL) 17  
 XX receptor like polypeptides useful as vaccines and in gene therapy. These  
 XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,  
 XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,  
 XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,  
 XX osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and  
 XX ophthalmological activities. The IL-17 receptor like nucleic acids and  
 XX proteins may be used to prevent and treat diseases associated with  
 XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These  
 XX include, for example immune disorders (e.g. inflammation, diabetes and  
 XX transplant rejection), infections (e.g. hepatitis and septicemia),  
 XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal  
 XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),  
 XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease  
 XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),  
 XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders  
 XX (e.g. stroke and atherosclerosis), cancers (e.g. leukaemia, myeloma and  
 XX breast cancer), reproductive disorders (e.g. infertility and  
 XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The  
 XX DNA and its complements may also be used as diagnostic probes to detect and  
 XX quantitate the presence of similar nucleic acids in samples and identify  
 XX patients needing restorative therapy. The IL17rlp may also be used as  
 XX antigens in the production of antibodies against the proteins and in  
 XX assays to identify modulators of expression and activity. The  
 XX anti-IL17rlp antibodies and antagonists may also be used to down regulate  
 XX expression and activity. This is the amino acid sequence of human  
 XX Interleukin 17 (IL-17) receptor like protein described in the method of

CC the invention.

CC Note: Residues 1-288 of this sequence correspond to residues 8-296 of the sequence shown in AAU10601 which is incomplete in the specification.

XX

50 Sequence 739 AA;

Query Match 92.3%; Score 3703; DB 22; Length 739;  
Best Local Similarity 93.7%; Pred. No. 0;  
Matches 704; Conservative 5; Mismatches 22; Indels 20; Gaps 3.

Qy 3. PMQLQSVFTVYVACNGSLQAVAGGSGRARGADTCGRMKAAARPRCLCVANEGVGPAS 62  
Db 9 PGSQOC-----CLHLDLGLGCVG-----RANLHLSAGSCS---LVFPQGVGPAS 48  
Qy 63. RNSGLNITFKYDNCITTYLNPVGRHVIADQNITISQYACQAVVAVTILSPGALGIEFL 122  
Db 49. RNSGLNITFKYDNCITTYLNPVGRHVIADQNITISQYACHQVAVTILSPGALGIEFL 108  
Qy 123 KGRVILEELKSEGRCQOQLILKDPKQNSFRKTGKESQPFNNMKFTDYFVKVVPFP 182  
Db 109 KGRVILEELKSEGRCQOQLILKDPKQNSFRKTGKESQPFNNMKFTDYFVKVVPFP 168  
Qy 183 IKNESNTHFFFTTRACDLILQDNLACKPFWKPRNLNISQSGDMQVSDFAHNFGR 242  
Db 169 IKNESNTHFFFTTRACDLILQDNLACKPFWKPRNLNISQSGDMQVSDFAHNFGR 228  
Qy 243 FFYLHLKHEGPFRRKTKCKEQTETTSCLLQNSFGDYIIELVDDNTTKRMHYALK 302  
Db 229 FFYLHLKHEGPFRRKTKCKEQTETTSCLLQNSFGDYIIELVDDNTTKRMHYALK 288  
Qy 303 PVHSPWAGPIRAVAITVPLVWISAFATLFTVMCKKQENIYSHLDESSSSTYTAALP 362  
Db 289 PVHSPWAGPIRAVAITVPLVWISAFATLFTVMCKKQENIYSHLDESSSSTYTAALP 348  
Qy 363 REELRPKPVLCYSKQGNHNVVOCFAVLODFCGCEVALDWEFSLCRGQREWY 422  
Db 349 REELRPKPVLCYSKQGNHNVVOCFAVLODFCGCEVALDWEFSLCRGQREWY 408  
Qy 423 IQIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELEFLVAVSAIAEKLQAQSS 482  
Db 409 IQIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELEFLVAVSAIAEKLQAQSS 468  
Qy 483 SAALSFIAYFDYSCEDVPGIILDLSTKYRLMDNLPQLCSHLHSDHGLQEPQHTROG 542  
Db 469 SAALSFIAYFDYSCEDVPGIILDLSTKYRLMDNLPQLCSHLHSDHGLQEPQHTROG 528  
Qy 543 SRNYSKSGSLVVAICNMQHQPIDEEDPWFEKQVPPHPPPLRYRPPVLEKFDGLVL 602  
Db 529 SRNYSKSGSLVVAICNMQHQPIDEEDPWFEKQVPPHPPPLRYRPPVLEKFDGLVL 598  
Qy 603 NDVCKPGPESDFCLVKEAAYLGATGPADSQHESQHGGLDQGEARPALDGSAAALPLLH 662  
Db 589 NDVCKPGPESDFCLVKEAAYLGATGPADSQHESQHGGLDQGEARPALDGSAAALPLLH 648  
Qy 663 TVKAGSPDMRDSGIYDSSVPSSLSPLMEGLSTDTQETTSLSSTESVSSGLGEEPP 722  
Db 649 TVKAGSPDMRDSGIYDSSVPSSLSPLMEGLSTDTQETTSLSSTESVSSGLGEEPP 708  
Qy 723 ALPSKLLSGGCKADLGRSYYTDELHVAPL 753  
Db 709 ALPSKLLSGGCKADLGRSYYTDELHVAPL 739

RESULT 15

ID ABB07630

XX ABB07630 standard; Protein: 739 AA.

AC ABB07630;

XX ABB07630;

XX 20-MAY-2002 (first entry)

DE Murine cytokine receptor, Zcytor18.

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Cytokine receptor; zcytor18; cell proliferation; antipsoriatic; human; pulmonary alveolar proteinosis; familial periodic fever; antitumor; erythroleukemia; chromosome 3p14.3; gene therapy; mouse.

Mus sp.

WO200208259-A2.

31-JAN-2002.

23-JUL-2001; 2001WO-US23253.

26-JUL-2000; 2000US-220747P.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Kuestner RE, Gao Z;

WPI; 2002-217048/27.

N-PSDB; ABA95037, ABA95038.

New cytokine receptor polypeptide designated zcytor18, useful for

inhibiting cell proliferation associated with psoriasis or tumor

growth, and modulating immune system by binding to endogenous zcytor18

ligand

Claim 1; Page 111-115; 119pp; English.

The invention relates to an isolated cytokine receptor polypeptide

designated zcytor18. The zcytor18 polypeptides can be expressed by

standard recombinant methodology. The polypeptides can be used to inhibit

cell proliferation associated with psoriasis or tumor growth. The

encoding nucleic acids are useful for providing zcytor18 in vivo by gene

therapy techniques. Zcytor18 oligonucleotide probes are useful for in

vivo diagnosis, and the zcytor18 probes and primers can be used to detect

and localize zcytor18 gene expression in tissue samples. The probes are

also useful for detecting gross aberrations in chromosome 3 in which

zcytor18 gene resides. The zcytor18 polynucleotides can also be used in

linkage-based testing of pulmonary alveolar proteinosis, familial

periodic fever and erythroleukemia, and erythroleukemia associated with

polymorphisms of cytokine receptors. The present sequence represents a

murine zcytor18 amino acid sequence.

Sequence 739 AA;

Query Match 84.4%; Score 3387; DB 23; Length 739;

Best Local Similarity 85.2%; Pred. No. 0;

Matches 645; Conservative 37; Mismatches 53; Indels 22; Gaps 6;

QY 1 MAPWLQCSVFTVYVACNGSLQAVAGGSGRARGADTCGRMKAAARPRCLCVANEGVGP 60

Db 1 MAPWLQCSVFTVYVACNGSLQAVAGGSGRARGADTCGRMKAAARPRCLCVANEGVGP 46

QY 61 ASRNSGLNITFKYDNCITTYLNP-VCKRVIADQNITISQYACHQVAVTILSPGALGI 119

Db 47 ASRNSGLNITFKYDNCITTYLNP-VCKRVIADQNITISQYACHQVAVTILSPGALGI 106

QY 120 EFLKGRVILEELKSEGRCQOQLILKDPKQNSFRKTGKESQPFNNMKFTDYFVKVVP 179

Db 107 EFLKGRVILEELKSEGRCQOQLILKDPKQNSFRKTGKESQPFNNMKFTDYFVKVVP 166

QY 180 FPSIKNESNTHFFFTTRACDLILQDNLACKPFWKPRNLNISQSGDMQVSDFAHNF 239

Db 167 FPSIKNESNTHFFFTTRACDLILQDNLACKPFWKPRNLNISQSGDMQVSDFAHNF 226

QY 240 GPRFFYLHLKHEGPFRRKTKCKEQTETTSCLLQNSFGDYIIELVDDNTTKRMHY 299

Db 227 GPRFFYLHLKHEGPFRRKTKCKEQTETTSCLLQNSFGDYIIELVDDNTTKRMHY 286

QY 300 ALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCKKQENIYSHLDESSSSTYTA 359

Db 287 VYKVSQSPWAGPIRAVAITVPLVWISAFATLFTVMCKKQENIYSHLDESSSSTYTA 346







GenCore version 5.1.4.p5.4578  
Copyright (C) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2003, 13:41:01 ; Search time 48. Seconds  
(without alignments)  
1508.109 Million cell updates/sec

Title: us-09-912-157-2  
Perfect score: 4013  
Sequence: 1 MAPK1QCSVFTVACLNG.....CQADLCGRSYTDELHVAAPL 753

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR\_73.1

1: piri:  
2: piri:  
3: piri:  
4: piri:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3005	74.9	564	2 T42695	hypothetical prote
2	170.5	4.2	846	2 T27282	hypothetical prote
3	126.5	3.2	718	2 T30113	hypothetical prote
4	117	2.9	757	2 T09081	telomere-associate
5	117	2.9	917	2 T04661	hypothetical prote
6	117	2.9	2946	2 T00867	hypothetical prote
7	116.5	2.9	901	2 F83781	transposase (8) /
8	115.5	2.9	938	2 I49071	protein kinase - m
9	115	2.9	998	2 S37627	protein-tyrosine k
10	110	2.7	535	2 T17212	hypothetical prote
11	110	2.7	592	2 I49239	vesicle transport
12	108.5	2.7	3788	2 T13960	beige protein homo
13	107.5	2.7	3942	2 T42730	Bassoon protein -
14	107	2.7	3788	2 T30851	lysosomal traffick
15	106.5	2.7	638	2 D86477	protein F1504.27 l
16	106	2.6	1448	2 A12007	Subtilase family p
17	105	2.6	901	2 JC6093	dead ringer nuclea
18	105	2.6	1571	2 T14155	zinc finger protei
19	104	2.6	1462	1 B36182	protein-tyrosine-p
20	103.5	2.6	663	2 A39897	GTPase-activating
21	103.5	2.6	930	2 A84668	Argonaute (AGO1)-1
22	102	2.5	813	2 B47485	ABR protein 2 - hu
23	102	2.5	859	2 A49307	98K GTPase-activat
24	101.5	2.5	822	2 A47485	ABR protein 1 - hu
25	101.5	2.5	1639	2 T50119	probable sensory t
26	101	2.5	641	2 T05497	hypothetical prote
27	101	2.5	664	2 T51247	ARR2 protein (impo
28	101	2.5	1275	2 A38985	nucleotide exchang
29	100.5	2.5	938	2 T05533	hypothetical prote

30	100.5	2.5	974	2 E59434	Rho GTPase activat
31	100.5	2.5	1007	2 T24643	hypothetical prote
32	99.5	2.5	857	2 E96949	serine/threonine p
33	99.5	2.5	794	2 E9089	213 protein - mous
34	99.5	2.5	981	1 F0WGM	gag-abl polyprote
35	99	2.5	341	2 H71716	190 kd antigen pre
36	99	2.5	783	2 A31491	sex-determining re
37	99	2.5	970	2 S63059	hypothetical prote
38	98.5	2.5	353	2 T33782	hypothetical prote
39	98.5	2.5	963	2 AD2381	type I site-specif
40	98.5	2.5	993	2 I48653	mouse developmen
41	98.5	2.5	1050	2 G86582	exodeoxyribonucle
42	98.5	2.5	1050	2 H72041	exodeoxyribonucle
43	98.5	2.5	1050	2 C81634	exodeoxyribonucle
44	98	2.4	526	2 T16124	hypothetical prote
45	98	2.4	820	2 S33794	hypothetical prote

## ALIGNMENTS

### RESULT 1

T42695 hypothetical protein DKFZp434N1928.1 - human (fragment).

C:Species: Homo sapiens (man)

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000 ~

C:Accession: T42695

R:Blöcker, H.; Boecher, M.; Brandt, P.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: 222230

A:Accession: T42695

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-564 <AAA>

A:Cross-references: EMBL:AL133097

A:Experimental source: adult testis; clone DKFZp434N1928

C:Genetics:

A:Note: DKFZp434N1928.1

Query Match 74.9%; Score 3005; DB 2; Length 564;

Best Local Similarity 99.8%; Pred. No. 8.5e-234;

Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	190	HPFFFRACDLILQPDNLACKPFWKPRNLNISQHGSDMQVSDPHAPNNGRFFFLHYK	249
DB	1	HPFFFRACDLILQPDNLACKPFWKPRNLNISQHGSDMQVSDPHAPNNGRFFFLHYK	60
QY	250	LKHEGPFRRKCKQBOETTTSCLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA	309
DB	61	LKHEGPFRRKCKQBOETTTSCLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA	120
QY	310	GPRAVAITVPLVWISAFATLFTVWCKKQENIYSHLDESSSTYTALPRELRER	369
DB	121	GPRAVAITVPLVWISAFATLFTVWCKKQENIYSHLDESSSTYTALPRELRER	180
QY	370	PRVFICYSSKDGQNNHNVQCFAYFLQDFCGCEVALDLWEDFSLCRGQREWIQIHES	429
DB	181	PRVFICYSSKDGQNNHNVQCFAYFLQDFCGCEVALDLWEDFSLCRGQREWIQIHES	240
QY	430	QPIIVVCSKGMKYPVDKKNYKHGGGSGKGEFLVAVSAIAEKLKQAKSSAALSXF	489
DB	241	QPIIVVCSKGMKYPVDKKNYKHGGGSGKGEFLVAVSAIAEKLKQAKSSAALSXF	300
QY	490	IAYVEDYSCGDVPGILDLSTKYRLMDNLPQLCSHLHSDRGHGLQEPQHTROGSRNYER	549
DB	301	IAYVEDYSCGDVPGILDLSTKYRLMDNLPQLCSHLHSDRGHGLQEPQHTROGSRNYER	360
QY	550	SSGSLSLVAICNNHQIDEPDWFQKVPHPPLRYEPVLEKFDGSLVNDVCKP	609
DB	361	SSGSLSLVAICNNHQIDEPDWFQKVPHPPLRYEPVLEKFDGSLVNDVCKP	420
QY	610	GPESDFCLKVEAAVYLGATGTPADSQHESQHGGLDQDGEARPALDGSAAALQPLLTVKAGSP	669

Db 431 GPSEDFCLVAYEAVTGATGCPADSGHESQHGGLDQGEARPDALDGSAAQLPILHTVKAGSP 480  
QY 670 SDMPROGDIYDSSVPSSELSPLMEGLSTQDTETSSLTESVSSSGISGEEPPALPKLL 729  
|||||  
Db 481 SDMPROGDIYDSSVPSSELSPLMEGLSTQDTETSSLTESVSSSGISGEEPPALPKLL 540  
|||||  
QY 730 SSGSKADLCGRSYTDDELHVAAPL 753  
|||||  
Db 541 SSGSKADLCGRSYTDDELHVAAPL 564  
|||||  
RESULT 2  
T27282  
hypothetical protein Y64G10A.e - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
C:Accession: T27282  
R:Alnough, R.  
submitted to the EMBL Data Library, September 1999  
A:Reference number: T20336  
A:Accession: T27282  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-846 <WIL>  
A:Cross-references: EMBL:AL110498; PIDN:CAB54470.1; CESP:Y64G10A.e  
A:Experimental source: clone Y64G10A  
C:Genetics:  
A:Gene: CESP:Y64G10A.e  
A:Introns: 106/1; 198/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3  
C:Superfamily: Caenorhabditis elegans hypothetical protein Y64G10A.e  
Query Match 4.2%; Score 170.5; DB 2; Length 846;  
Best Local Similarity 21.1%; Pred. No. 3.3e-05;  
Matches 141; Conservative 82; Mismatches 225; Indels 211; Gaps 37;  
QY 99 QYACHDOAVTILSPGALGTEFLKGRVILELSEKQCOOLIKDPKOLNSFRGTG 158  
Db 294 QY-CFEEYVRLDS--GIVMQSALITKDELRT-----IINGRPVQGEF----- 338  
QY 159 MESOPFLNMKFTDYFVKVPPFPKINNESYHPFFTRACDLILQPNLAC-KPFWKPR 217  
Db 339 -----NETDIEDTLIPSVIESAHD-----GRC-LCVTENGCSCLAADNKPV 382  
QY 218 NLMSIQSGSDMOVSPDHAPHNGRFYLVKLKHEGPKRKTCKOETTTSCLLQNV 277  
Db 383 KLP-----RIEKPPATSN-----QTESDGAKEDKEDTTWT----- 415  
QY 278 SPGDYIELVDOTNTRKVMH-YALKPVHSPMAGPIRAVAITVPLVWISAFATL--FTVM 334  
Db 416 -----WHTYA-----ITGAILAILFILSVCAGLKCYKFF 445  
QY 335 CRKQOENIYSHLDSESSSTYAAALPRELRPRPKVFLCYSSKDGQNHNVVOCFAF 394  
Db 446 NKKKASNI--HLLNENPAFS-HSGSPL-ILKQISLVLIYV-SHDSQAHEAVLAFAEL 500  
QY 395 LQDFCCGVALDQWEDFSLCQEGRENVIOKHESOFIIVCSKGMKYFDVKNNYKKG 454  
Db 501 LRDVFNVLHVDWDEDDI--EENRAEYINSIVRANKVIIINSIG-AYF--RTVFRHOR- 555  
QY 455 GRGSGKGLFVAVSAIAEKLRQAKQSSAALSFKFIATFYDSCBGDV--PGIOLDSTKY 512  
Db 556 -----EPATERITTCRND-----VIFDMQCELALQHPCVISCFESY 591  
QY 513 -----RLMD-NLPQLCSHLHSDHGLQEPQHTQCRSRNRYFRSKSGSLVAVI 560  
Db 592 TNPKYVFFPINLQYSIP---NSLMTWTALTQEPARPEQLAGNQVFAF-----LQAAI 644  
QY 561 CNMHQFIDEEPWFKE-----QVFPFPPPLRYR----- 589  
Db 645 SRKLNATIESDPQWQHNVTHVATRVSELAHNIVPL-PPSLEVKEDEDAFGQMETLPI 703  
QY 590 EPVLEKF-----DSGLVNDVMCKPESDFCLAVEAIVLGATGPADSGHES 636  
|||||

Db 704 DELKEKFAAKRDLEVEVLDSKLLKEDVKCAPGP-----IHVETPEVLEPAEPMEE 758  
QY 637 QHGGLDQGEARPDALDGSAA---LQPLL-HVVKAGSPDMRPSGIYDSS-VPSSELS 689  
|||||  
Db 759 ABEED-EBEDDDVDVSGEOTARIELQRLIVH-----KDNHDSGNLAYSVSGSDFS 809  
|||||  
RESULT 3  
T30113  
hypothetical protein F56D1.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C:Accession: T30113  
R:Chisoe, S.; Wilson, R.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid F56D1.  
A:Reference number: T20737  
A:Accession: T30113  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-718 <CHI>  
A:Cross-references: EMBL:U39997; PIDN:AAA81100.1; CESP:F56D1.2  
C:Genetics:  
A:Gene: CESP:F56D1.2  
A:Introns: 93/1; 121/2; 163/3; 459/1; 517/3; 555/1; 615/3; 667/3  
C:Superfamily: Caenorhabditis elegans hypothetical protein F56D1.2  
Query Match 3.2%; Score 126.5; DB 2; Length 718;  
Best Local Similarity 21.1%; Pred. No. 0.091;  
Matches 82; Conservative 64; Mismatches 149; Indels 94; Gaps 19;  
QY 363 REELRPRP-----KVELCYSSKDGQNHNVVOCFAFVLFQDFCGCEVALDLWEDFS 412  
Db 398 RDKVRSREVRNIALTEFKVVIYAD-DNDLHTDCVKKLVENLNCASCPVDEKLIT 456  
QY 413 LCREGOREWVOKTHESQFIIVCVSGMKYFDVKNNYKKGGRSGKGEFLVAVSAIA 472  
Db 457 AEQIVPSRMLVDQILSSLUKKFIIVVSDCAEKILDTSEATHQLVQARFADLFGPAMEI- 515  
QY 473 EKLQAKOSSAALSFKFIATFYDSCBGDV---GILDSTKYRLNDNLQPLCSHLHSD 529  
Db 516 --IRDATHNEPARKKAVVRENTS--PHVPPNLAAILNLPT-FILPEQFAQLTAFLHNYE 570  
QY 530 HGLQEPQHTQGRNRYFRSKRSLSY---VAICNMHQFIDEEDPFKQFVP----- 580  
Db 571 H-----TERANTONISEAQIHENWILCASRMMSFFVRNPWNLETRWPKDELAA 619  
QY 581 PHPPPLRYREPVLKEDFSLVNDVMCKPESDFCLKVEAAVILGATGPADSGHESQHG 640  
Db 620 LH---LKRQSPVIVPIQT-----EED---RIAAIKYNLVPQALVDS--- 657  
QY 641 LQDQGEARPDALDGSAAQLPILHTVKAGSPDM--PRDSGIYDSSVPSSELSPLMEGLST 698  
Db 658 -DED-----DVIDLP--HASHQNPILILPPEQCG-----PDS-SD 690  
QY 699 DQETSSLTESVSSSGISGEEPPALPK 727  
Db 691 SEDSSSESESESONEG---EDPKTIVVK 716  
RESULT 4  
T09081  
telomere-associated recQ-like helicase - smut fungus (Ustilago maydis) (fragment)  
C:Species: Ustilago maydis (corn smut)  
C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-May-2000  
C:Accession: T09081  
R:Sanchez-Alonso, P.; Guzman, P.  
Genetics 148, 1043-1054, 1998  
A:Title: Organization of chromosome ends in Ustilago maydis: recQ-like helicase motif  
A:Reference number: 216557; MUID:98198830; PMID:9539423  
A:Accession: T09081  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

A:Residues: 1-757 <SAN>  
 A:Cross-references: EMBL:AF030885; NID:92642221; PID:92642222  
 A:Experimental source: strain PB2  
 C:Genetics: T04661  
 A:Gene: UTASRECQ  
 C:Keywords: DNA binding

Query Match: 2.98; Score 117; DB 2; Length 757;  
 Best Local Similarity 20.48; Pred. No. 0.57;  
 Matches 111; Conservative 56; Mismatches 187; Indels 190; Gaps 27;

QY 268 ETTSCLLOWSPCDYIELVDVNTTKVMYALKVHSPWAGPIRAV---ATVPL--- 321  
 DB 77 ETILIPVALRANKLADVRA---IRHWQP-GSKAAPVLVSTEAATLAFKE 131  
 QY 322-----VVISAPATLFTVMCKKQOENIYSHLDESSSESYTAALP----- 362  
 DB 132 YANRLQOORLDRIVIDECLTLTARSYRSMQLAHVRDETQVMTLTLPIPEDA 191  
 QY 363 --RELRPRKVF-----LCYSSKDGONHNVVOCF-AVFLDFGCGEVALDLWEDF 411  
 DB 192 FISHNKLTPLVIRESTRNSNLCSYVTAERMSGHTCYDAVRVD---ECRARTDIW--- 246  
 QY 412 SLRCQOREWVQKTHESQFIIVVCSKGMFYVDK-----KNYKHGGGRGS----- 458  
 DB 247-----NGORD-----RIIVYCTS--KELVARLAEMLGOAAYSSSGSEADKAAIIQ 290  
 QY 459 ---GGGELFLVAVAIAEKLRQAKSSAALSFKFIAYFYDSCGDPVPGIL--DLSTKY 512  
 DB 291 DWICGKSPVIATSA-----LGVGFDPHYRFVHLLGLDLITDF 331  
 QY 513 -----RLADNLPOLCSHLHSRDRHGLQEPGQHTROGSRNFRS 550  
 DB 332 SQSGRAGRGMPASILLAGQLDDRAP-ASGKASSAEKGVAPG---ADKEMQLYRS 387  
 QY 551 KSGRSIYAICNMHGFIDEEDPWFKEQVFPFPPPLRYREPVLEKFDSCGLVNDVMCKPG 610  
 DB 388 RK-----YCLRGVLSQLIDQRSDW-----RWCEGDLQCSVC 419  
 QY 611 PESDFCLKVEAAVLGATPADSOH---ESQHGGLDQGEARPALDGSAAOLOPLRLTKAG 667  
 DB 420 PGHFP-----QARGPGQPFHTAPAGDPSTQGRHPSMGSS--HPSMH----- 463  
 QY 668 SPDMPRDSGIYDVSPPSE-LSLPLMEGLSTQDTETSSLTESVSSS---SGLGEEPEPA 723  
 DB 464 -----GSSHPSSGSHSPSINGSSHPSSINGSS--HPSINGSGHGQGRKQOOPD 510  
 QY 724 LPSK 727  
 DB 511 PPSE 514

## RESULT 5

T04661  
 hypothetical protein F8D20.70 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 24-Nov-1999  
 C:Accession: T04661  
 R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Meves,  
 submitted to the Protein Sequence Database, July 1998  
 A:Reference number: Z15361  
 A:Molecule type: DNA  
 A:Accession: T04661  
 A:Residues: 1-917 <BEV>  
 A:Cross-references: EMBL:AL031135  
 A:Experimental source: cultivar Columbia; BAC clone F8D20  
 C:Genetics:  
 A:Map position: 4  
 A:Introns: 13/3; 58/2; 93/1; 274/3; 340/3; 373/3; 395/1; 437/3; 536/1; 624/2; 665/3; 685/3  
 A:Note: F8D20.70  
 C:Superfamily: Arabidopsis thaliana hypothetical protein F8D20.70

Query Match 2.98; Score 117; DB 2; Length 917;

Best Local Similarity 18.38; Pred. No. 0.76;  
 Matches 167; Conservative 130; Mismatches 296; Indels 320; Gaps 42;

QY 19 NGSQAVAGSGRARGADTCGRM--KAAAPR-----LCVANGV----- 58  
 DB 92 NGSRSV-----GYSNG-DILWSPSGECSPSSAMICKNLNGLYSEKPIASLKWY 145  
 QY 59 --GPASR-----NSGLYNITFYDNCCTYLPVGHV---IADAQNI--TISOYACHDQ 105  
 DB 146 ABGKASRVYVIGSSNSLQVLLNEQTETRMIKGLHVSEPCADMEMIADVNEQSKHQ 205  
 QY 106 VAVTILSPGALGI--EFLAGFVILEELKSGCQOOLILKDPKOLNSSFKRTGMSOP 163  
 DB 206 DFLFVLGSGRVAYDYMIEKLIQOSKSPSLPKETVTVVLLPFDSSSITVKGKFLWP 265  
 QY 164 --FLMKFETDY-----FVKVVPFPIKNSN---YHPFF-----FRTRACDLLQPD 206  
 DB 266 SHLLNLSDE-DYAOQLAKDAVFPFHTVPKSSSAHPFGFTKVNVIYITGCHDGTISW 324  
 QY 207 NLACK-----PFMKPR-NLNIQHG-----SDMOVSDHAPHNFGFRFFLYH 248  
 DB 325 DMTCSFPILVLEKEIDQDVSSRGNALTAHYDSNRLVSGDHNGKVLRYRFPPEY 384  
 QY 249 KLKH-----EGPFR-----KTCQEQTTTSCLLQNVSP-----GDYIELV 287  
 DB 385 LTENSFIPFGSLKGNHIVQSVYIKLTGTCIQKSONSKHLAIGSDQGHDSLVEVI 444  
 QY 288 DOTNTRKVMYALKVHSPWAGPIRAVAITVPLVVISAFATLFT----- 332  
 DB 445 D-----ALTPV-----LQVSLVDIEENNVLYTKHIASDICPGIISLQ 482  
 QY 333 -----VMCKKQOENIYSHLDESSSESYTAALPRELPRPKVFLCYSKD 380  
 DB 483 FSCIVQGFERNLVAMRDSSVFA-LDSDTGNMIGTNMKP-----KPKVLYHQIILD 536  
 QY 381 GQNHNVVQCFAYFLDFGCGEVALDLWEDFSLCREGREWVIOKIHESQFIIVWCS--- 437  
 DB 537 GK-----QDTSG-----NGFOTSRES-----TVBEISITROPSVLVCSKA 571  
 QY 438 -----KGMKYFVDKKNYKHG-----GGRSGKGLFLVAVAIAE-----K 474  
 DB 572 IYIYSLAHVQGVKVLHKKFKSSPICSNASTFYGTSGVG---LTLYTDTCTVEISLSE 628  
 QY 475 LRAOKS-----SSAALSFKFIAYFYDSCGSD-----VPGIOLSTKRLMD 516  
 DB 629 LSQAKQTSIRGFTYSSPKNSLPETITASWDGLVMVNGDDELIVSVLPQKETFRLYE 688  
 QY 517 NLPOLCSHLHSRDRHGLQEPGQHTROGSR---NYFRSKSGSLVAVAICNMHOFIDSE 570  
 DB 689 SM-----NRVYKDNVCHEGIIITSSSPREKKNMFGSVFKTKRRTDTPESSKETIEL 744  
 QY 571 PMFKEQVFP-----HPPPLRYREPVLKFPDS 598  
 DB 745 SKIFSTANPWNNNVNSREINTITRVEDEEELDDIDDDHHPNQQOQEKREOGILS 804  
 QY 599 GL-----VLNDVMCKPGPESDFCLKVAALVAGATGADSOHESQHGGL----- 641  
 DB 805 GLSKQMANRESNFKGLKQMAKNEKSVV---NDEKHEEKNGATVQIKKKGFTSS 860  
 QY 642 DQDGEARPALDGSAAOLOPLLHTVAKGSPDMPRDSDGIYDSSVSPSELSLPLMEGLSTQDT 701  
 DB 861 DEMGAAKMA-----QSKLQD-----NLKKGLOISLRTT 888  
 QY 702 ETSSITESVSSSS 714  
 DB 889 EMDTAKSFESTA 901

## RESULT 6

T00867  
 hypothetical protein At2g45540 [Imported] - Arabidopsis thaliana  
 N;Alternate names: hypothetical protein F17K2.7  
 C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 16-Feb-2001  
C:Accession: T00867; G84891  
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,  
submitted to the EMBL Data Library, March 1998  
A:Description: Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence.  
A:Reference number: F14207  
A:Accession: T00867  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2946 <RDB>  
A:Cross-references: EMBL:AC003680; NID: g2979540; PID: g2979554  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;  
Euse, D.; Hierman, W.C.; White, O.; Eisen, J.A.; Zilberberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Sequence number: A84420; MUID: 20083487; PMID: 10617197  
A:Accession: G84891  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2946 <STO>  
A:Cross-references: GB:AE002093; NID: g2979554; PID: AAC06163.1; GSPDB: GN00139  
C:Genetics:  
A:Gene: F17K2.7; At2g45540  
A:Map position: 2  
A:Introns: 652/1; 913/3; 1165/3; 1210/3; 1283/3; 1245/3; 1309/2; 1336/3; 1438/3; 1638/2;  
; 2449/2; 2481/3; 2643/1; 2890/3; 2931/3  
Query Match 2.9%; Score 117; DB 2; Length 2946;  
Best Local Similarity 18.7%; Pred. No. 4.3;  
Matches 164; Conservative 105; Mismatches 314; Indels 294; Gaps 40;  
QY 2 APTQLQCSVFETTNACLSQAVAGGSGRAGADTCGRMKAAARPLCVANEGVCPA 61  
DB 333 ATWIIYIESPADTNAATAAATAAANA---AKSGKTSAMSAANAAS---ALAGEG--- 441  
QY 62 SRNSGLNITFKYDNCNTYLNPGKHVIADAQNTISQYACHDOVAVTILWSPGALGIEF 121  
DB 442 ---TAHMPRLSFLSADNOGIEAFHA--- ---OF 467  
QY 122 LKGFVRILEELKSEGR--- ---QC--- ---QQLIKDPKQLNSFKRTG 158  
DB 468 L-----VVEGSGKGRKSSLHFAKPCQWYFGLSEKCKQLLKAESLRLIDGSL 522  
QY 159 MESQFLMKFTDYFKVVPVPPSIKNSNTHPEFF-----RTRACOLL 202  
DB 523 YESRPF-----DFPRISK-----PLSFCCIGTNPPTMAGLQRRRCQPLF 563  
QY 203 LQ--PDNLACKPFWKPRNLNISOHSDMOVSFDHAPHNFGFRFFYLHYKLKHEGPKRKT 260  
DB 564 AEMGPVYIFKEPIGPERMARLASRGDVLPCFGNGA---GLPWLATNDIVRN----- 612  
QY 261 CKOQTETYS-----CLLQNVSPGDYIIEVDNTTKK-----VMHYA-- 300  
DB 613 -KAESILLADIGGTHLLYHPCLLSGRFCPD---ASLSGAAGTLRRRAEVLGQVHYATR 669  
QY 301 LKPVHSPWA---GPRAVAIVT-----PLVVISAFATFTVM--- 334  
DB 670 MKPVESWALAYGPNLSPLTVSVVHKDLSLEPCLNPLSLSTVTLAAPVRINSVAIQ 729  
QY 335 -----CRKQOE---NIYSHDEESSESTYTAALPRERLPRPKVFLCYSSKQCN 383  
DB 730 HPGNNEELCTQCPFEILARILSLIHLASLORKHGDVGGEEL--VAATVSLQSQK--IN 786  
QY 384 EMNVVQCFAFYLODFCCCEVALDLWEDFSLCREGQEWYQKIHESQFIIVVCSKGM-- 441  
DB 787 HVLKVLQFRTLLD-----LKIN--SLCNYGLQKLLSSLDQNVFTFATAMDAEAI 836  
QY 442 -----YFVDKKN-----YKHGGGSGKGLFLVAVSAIAEKLROAKQSSAA- 485  
DB 837 QLLIDGCRRCYMWISEKSETTFPLDGNTRONGELNALIDELLVITELLMGAASPLAAD 896

QY 486 -LSKEIAVTFDYSCEDVPGVILDLSTYRLMDNL---POLCSHLHSDRHGLQE---PQOH 538  
DB 897 DLRELGLFIIDSPQNVQVAVLHLYLVQPNARAQMAFVETTSIGTETLLVLORE 956  
QY 539 TROGSRNRTFRSGRSLSVAICNMHOFIDEEPWFKEKOFVFFHPPLRYREPVLKFD 598  
DB 957 ARTGEDNVLMGRSGKR-----SSTDPSSEKS--PIN-----ESGSVKQLDS 995  
QY 599 GLVLNDV-MCKPQPSDFCLAVEAALVGAAG-PADSOHESQHGGLDQGEARPALDGSAA 656  
DB 996 NPHDNEIGFDLPGDGN---SVEDDNYGSLNVPESYRQKEHG----- 1035  
QY 657 LQPLHLYTVRAGSPDMPROSGIYDSSVPSSELSPLMEGLSTDOETSETLSVESSSSGL 716  
DB 1036 -----STPVVCDSDSVSISNINIRLS-----AEIGGISLSISADSAR 1074  
QY 717 GE-----EEPPA-----LPSKLLSSGCKRADLGCRS 742  
DB 1075 NNVTYNDNSDAVVVGIIRLIGALISSGHLTFDFDARS 1111

RESULT 7  
F83781  
transposase (08) / ABC transporter (ATP-binding protein) BH1054 [imported] --Bacillus  
C:Species: Bacillus halodurans  
C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: F83781  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a  
A:Reference number: A83650; MUID: 20512582; PMID: 11058132  
A:Accession: F83781  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-901 <STO>  
A:Cross-references: GB:AF001510; GB:BA000004; NID: g10173440; PID: BAB04773.1; GSPDB: G  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH1054  
Query Match 2.9%; Score 116.5; DB 2; Length 901;  
Best Local Similarity 19.6%; Pred. No. 0.82;  
Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;  
QY 61 ASRNSGLNITFKYDNCNTYLNPGKHVIADAQNTISQY-ACHDOVAVTILWSPGALGI 119  
DB 333 ALKESGL-----PLPKTLIADAGYSGESNYVAVADELTFETCTPS----- 371  
QY 120 EFLKGFVRILEELKSEGR-----OCQOL--ILKDPKQLNSFKRTGMSQPLANKF 169  
DB 372 ---HTR--QEQKRFAKREHPYNWCRDETDVYWCNQRKVSFKRYTKTDY---GY 423  
QY 170 ETDFYV-----KVYFP-PSI-----KNESNYHPPFFRTRACDLLLQDNLKAPFWKPR 217  
DB 424 ARDFKYECESCEGCPFPPECTKARGNRQVHNPVY-----BELKAKQHKLK 471  
QY 218 NLMSIQHG-----SOMQVSFDHAPHNFGFRFFYLHYKLKHEGPKRKTCKOEQTET 269  
DB 472 ---SEGRTLQYKRTKTDVESVFGHVQNLGFRRLHKG----- 507  
QY 270 TSCLLQNVSPGDYIIEVDNTTKKVMHYALAPVHSPWAGPIRAVAIVTLPVLVIS-AFA 328  
DB 508 -----ESVHIELGLVALANLR 524  
QY 329 TLFVTKRCKKQOENTYSHLDEESSESTYTAALPRERLPRPKVFLCYSSKQGNHNVV 388  
DB 525 KRATVRRSKPEKNTNQHKNEN-----RIKRE-----SREYVL 558  
QY 389 QCF---AYLQDFCCCEVALDLWEDFSLCREGQEWY-----IQKHESQFIIVVCSKGM 441  
DB 559 KCFWDSFFIKSGQKQYASFAFD--KLREGGENMIEVILSKTYRRQV-----KGIN 612  
QY 442 YFVDKKNYKHGGGSGKGLFLVAVSAI-----AEKLRQAKSSSAAALS 488

Db 613 MEIRGENVGLGPGAGKSTTSMISLIQPTSDVLKGGSHKQAKRSILGVVPO 672  
 QY 489 FVAVFDYSCS---GDVPGILDSKYRLMNLPLCSHLSRHDGLQEPGHTROG 542  
 Db 673 EIVAVHDITARENAFFGKTYGLKGEELKHR-MESTLQLV---GLEE---RON 718  
 QY 543 SRNFRSKRSRSLYVAICNMHO---FIDEEP 571  
 Db 719 DRVHTFGGKRLNINAVALLHEPELLINDEP 750

RESULT 8  
 I49071  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 18-Jun-1999  
 C:Accession: I49071  
 R: Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.  
 Mech. Dev. 48, 153-164, 1994  
 A:Title: Identification of novel protein kinases expressed in the myocardium of the developing mouse  
 A:Reference number: I49071; MUID:95200798; PMID:7893599  
 A:Accession: I49071  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-938 <RES>  
 A:Cross-references: EMBL:U11493; NID:g595418; PIDN:AAAG7925.1; PID:g595419  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C:Keywords: ATP; transmembrane protein  
 F:571-839/Domain: protein kinase homology <KIN>  
 F:579-587/Region: protein kinase ATP-binding motif  
 F:862-928/Domain: SAM homology <SAM>

Query Match 2.9%; Score 115.5; DB 2; Length 938;  
 Best Local Similarity 19.4%; Pred. No. 1;  
 Matches 160; Conservative 120; Mismatches 285; Indels 259; Gaps 45;

QY 9 SVFTVNAACL-NGSLAVA---AGSGR---ARGADTCGRKMAARPLC----- 52  
 Db 170 SLIVAPACIANAVESVPLKLYCNGDGMVPGACTCATGHEPAKESQCRACPPGSY 229  
 QY 53 VANEGVGA-----SRNSG-----LYNITFYDN-----CTTYLNPVGRKHVIAAQ 93  
 Db 230 KAKQEGPCPCPNSTTSPAASICTCHNFRADSDADSACTTRSP-PRGVISNV- 287  
 QY 94 NITISYACHDOAVTILNS-PCALGIEFLKGFVILEELK-SEG-----RQCOOLIL 144  
 Db 288-----NETSLILENSEPRDLGDRDILLYNVICKKRGSGAGGPATCSCDDNVE 337  
 QY 145 KDPKOLNSFRKTOMESQPLNKKFTDYFVKVFPFSSIKNESNYHFFFTTRACDLILQ 204  
 Db 338 FVPROGLTERRVHS-----HLLAHTRTFEVQAVNGVSKSPLPRYAANVITTNQAA 392  
 QY 205 PDNLACKFPKPRNLNLSQHSQDMOVSFOHAPHNGPREFYLVHKLKHEGPF-KRKTCKQ 263  
 Db 393 PSEV-----PTLHSHSTSGSSLTSLSWAPPERNG-----VILDYEMKY---FKSKAIAS 439  
 QY 264 EYTTETTSCLQNVSP-GDYIIELVDVDDVNTTRKY-----MHYALKPVHSPNAGPRAVA 316  
 Db 440 TVTSOKNSVQLDGLQDPAHYVQV-----RARTVAGYQYTHPAEFETTSERGSGAQQLQ 494  
 QY 317 ITVPLVLTSAFA-----TLTVNCRKQENIYSHLDEESSESTYTAALPRERLRP 368  
 Db 495 EQLPLVGSNVAGFVFWVVVVVIAVLCKLRQH-----CPDAEYTEKL-QQYIAP 543  
 QY 369 RPKVFLCYSKDQGNHNVQCFAYFLQDFC-GCEVALDLMEDFSLCREGREWYQKTH 427  
 Db 544 GKNVYIDPTFYEDPN--EAVREFAKEIDVSKVIEVIGAGEFGEVCR----- 589  
 QY 428 ESQFIIVVCSKGMKYFDYKKNYKKGSGKGLFLVAVSAI-----AEKLRAQKSSS 483  
 Db 590-----GRLLPGRREV-VAKTLKVGYTERQRDFLSA 623

QY 484 AALSKEFIATVFDYSCGDPVGGILDLS---TKYR-----LMDNLPLCSHLSRHDGLQ 533  
 Db 624 SNMQCF-----DHPNIIIRLEGVYKSRVPMILTFEMENC-ALDSFLRLND----- 667  
 QY 534 EPGQHT-----RQSGRRNY-FRKSGRSLYV---AIC-----NMHQFIDE 569  
 Db 668---GQFTVQLVGLRGIAAGKYLSEMYVHRDLAARNILVNSLVCKYSDFGLSRFLFD 725  
 QY 570 EPDWFKEQF-----VPEH---PPPLYRFPVLEKFDG-----GLVINDVMCKPGPE 612  
 Db 726 DPS--DPTVTSSILGGKIPIRMTAPEIAYR-----KFDASDWSYGIWMEVMS----- 773  
 QY 513 SDFCLKVEANVLCATGCPADSGHESQGLDQDGEARPDLDGSAALQPLLLHTYKAGSPSDM 672  
 Db 774-----YGEQPYMNSNQDDINAVEDYRLPPMDCTPALHQLMASCWDRMLR 822  
 QY 673 PRDSGIYD-----SSVPSSELSLPIAMEGLSTDOT 701  
 Db 823 PKFSQIVNTLKLIRNAASLKVATASAPSG-MSQPLLDRTVPDYT 865

RESULT 9  
 S37627  
 C:Species: Homo sapiens (man)  
 C:Date: 19-May-1994 #sequence\_revision 03-Aug-1995 #text\_change 04-Feb-2000  
 C:Accession: S37627  
 R: Boehme, B.; Holtrich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.; Ru  
 Oncogene 8, 2857-2862, 1993  
 A:Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.  
 A:Reference number: S37627; MUID:93390963; PMID:8397371  
 A:Accession: S37627  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-998 <BOE>  
 A:Cross-references: EMBL:X75208; NID:g406867; PIDN:CAA53021.1; PID:g406868  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea  
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein  
 F:631-859/Domain: protein kinase homology <KIN>  
 F:639-647/Region: protein kinase ATP-binding motif  
 F:922-988/Domain: SAM homology <SAM>

Query Match 2.9%; Score 115; DB 2; Length 998;  
 Best Local Similarity 19.0%; Pred. No. 1.3;  
 Matches 159; Conservative 122; Mismatches 301; Indels 250; Gaps 42;

QY 35 GADTCGRKMAARPLC-----VANEGVGA-----SRNSG-----LYNITFK 73  
 Db 267 GACTCATGHEPAKESQCRPPGSKAKQEGPCPCPNSTTSPAASICTCHNFR 326  
 QY 74 YDN-----CTTYLNPVGRKHVIAQNTITISYACHDOAVTILNS-PCALGIEFLKGR 126  
 Db 327 ADSDSADSACTVPS-PRGVISNV-----NETSLILENSEPRDLGVRDLDLYN 374  
 QY 127 VILEELSEG-----RQCOOLILKDPKOLNSFKRTGMESQPLNKKFTDYFVKVFP 181  
 Db 375 VICKKHGAGASACRCDNVEFVPROGLISEPRVHS-----HLLAHTRTFEVQAVN 429  
 QY 182 SIKNESNYHFFFTTRACDLILQDNLACKFPKPRNLNLSQHSQDMOVSFOHAPHNGF 241  
 Db 430 GVSKSPLPRYAANVITTNQAAPEV-----PTLHSHSTSGSSLTSLSWAPPERNG- 481  
 QY 242 RFFVLHKLKHEGPF-KRKTCKQEOTTTTSCLLQNVSP-GDYIIELVDVDDTTRKVMHY 299  
 Db 482--VILDYEMKY---FKESGIASITTSQNSVQLDGLRDPARYVQV-----RARTVAGY 531  
 QY 300 A--LKPVH-----SPWAGPRITAVITVPLVVISAFATL-----FTVMCRKKQENIYS 345  
 Db 532 QOYSRPAEFETTSERGSGAQQLQEQPLIVGSATAGLVFVAVVIAVLCKLRQH----- 587  
 QY 346 HLDEESSESTYTAALPRERLRPKVFLCYSKDQGNHNVQCFAYFLQDFC-GCEVA 404  
 Db 588-----GSDSEYTEKL-QQYIAPGMKYIDPTFYEDPN--EAVREFAKEIDVSKVIEV 638

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QY 405: LDLWEDFSLCRGQREWYOKIHESOFILVCSGKMKYFVDKKNYKHGGGRSGKGELF 464
Db: 639: LGAGEFGEVCR-----GRLKQPGRGREV 661
QY 465: LVAYSAT----AEKLRQAKSSAALSFKIAYFDYSCGDVPGILDLS---TKYR---- 513
Db: 662 --VALTKLVGYTERQRDFLSEASINGQF-----DHPNIIRLGCVTKSPWMI 709
QY 514: ---LMDNLQGLCSHLSRDHGLQEPQHT-----RQGSRRNY--FRSKSR 554
Db: 710: LTFENEMC--ALDSFURLND-----GQFTVLQVLMRLGIAAGMKYLSMMYVHRDLAAR 762
QY 555 SLKY---AIC-----NMHQFIIDEEPWFQKQVFPFHP-----PLRYREP---VLEKDF 597
Db: 763 NILVSNLKVCKYSDPGLSRLEDDPS-----DPTTYSLLGCKIPIRWTAPEAIARVKT 816
QY 598 S-----GLVLNDVCKPCPFSEDFCLKYEAIVGATGADSOHESQBGGLDODGEARPA 650
Db: 817: SASDWSYGIWVMEVMS-----YGERPTWMSNDQVINAVEQDYFLRPP 860
QY 651 LDGSNAQLPILITVKAKSPMDPSDGIYDS-----SVPSSLSLPLMUGEL 696
Db: 861: MDCETALHQLMDCWVRDNLRLKFSQIVNTLDKLIRNAASLKVTASQAQSGMSQPLDRT 920
QY 697 STDQTTSLTSSVSSSGLGEPEEPALPKLLSSGCKADLCGRSYDEL 747
Db: 921: VPDYTTTFTVGDWLDAIK--MGRYK-----ESFVSACGFSDLVQMTAEDL 965

RESULT 10
T17212
hypothetical protein DKFZp434P211.1 - human. (fragments)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17212
R:Poustakka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wilmann, S.
submitted to the Protein Sequence Database, September 1999
A:Reference number: 218723
A:Accession: T17212
A:Status: preliminary
A:Molecule-type: mRNA
A:Residues: 1-486;489-535 <POU>
A:Cross-references: ENBL:AL117401
A:Experimental source: adult testis; clone DKFZp434P211
A:Note: the cDNA sequence contains a 1 frameshift near codon 488
C:Genetics:
A:Note: DKFZp434P211.1

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RESULT 11
149239 vesicle transport protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49239
R:Tellam, J.T.; McIntosh, S.; James, D.E.
J. Biol. Chem. 270: 5857-5863, 1995
A:Title: Molecular identification of two novel Munc-18 isoforms expressed in non-neur
A:Reference number: I49238; MUID:95197608; PMID:7890715
A:Accession: I49239
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-592 CRES#
A:Cross-references: EMBL:U19521; NID:g642027; PIDN:AAA69913.1; PID:g642028
C:Genetics:
A:Gene: munc-18c

Query Match 2.7%; Score 110; DB 2; Length 592;
Best Local Similarity 18.5%; Pred. No 1.5;
Matches 93; Conservative 64; Mismatches 157; Indels 188; Gaps 22;

QY 321 LVVISAFATLFTWCKKQQ-----ENIYSHLDESSSTVTAALPRERLRPK 371
Db 34 IMLDEFITKLSSCKMTDLLEGIIVNIYKNEPVQMKALYF-----ISPTPK 86
QY 372 VFYCYSSKDGQNMNVQCFAYFLQDFC-----GCE----- 402
Db 87 SVDCFRLDRFGSKSEKKYKAAYIYTFDCPSDLFNKIKASCSIRRCKEINISFIPQESQ 146
QY 403 -VALDLNDFELC-----RQGEWYIQIHESQFIIVVC-----SKGKY----- 442
Db 147 VYTLDPDAFYCYSPDSNASRKEVYNAEQ--IVTVCATLDENPCVRYKSKPLDNA 204
QY 443 -----FVQK---NTK--HKGGRGSGKGLFLV-----AVSAIAEKLQAKQSSAALS 487
Db 205 SKLAQVKEKKLEDYTKIDEKGLIKGTQSQLLIIDRGFPVSTVLHEL----- 252
QY 488 KFTAVYFD-----YSCG-DVPGIL-----DLSTKYR-----LMDNLPLQCSHLH 526
Db 253 TQQAMAYDLLPTENDTYKYKTDGKEAIVLEDDDLVWRVRRHRIAVYLEEIPKLMKEIS 312
QY 527 SRDHGLQEPQHTROGSRNFRFSKRSYIVAI CNHQFIDEEPDTFKQFPVPPPL 586
Db 313 STK-----KATEGTSLSALTQLMKKMHPFRKQISKQW-----HL 348
QY 587 RYREPVLEKF-----DSGLVLNDVMYCKPGPESFCLAVE 620
Db 349 NLAEDCMNFKLNIEKCKTQDIALQDAEQGRVKDSMLVLLPVLL--NKNHNDCKIR 406
QY 621 AAVLGATGPADSQESHGGLDQGEARPALDGSALQPLLTHTKAGSPDMRPD-SCII 679
Db 407 AVLLIYFGLNGTEEN-----LDRLIHNVKIEDSDMIRNWSHLG 446
QY 680 DGSVPSSLSPLAMEGLSTQDT 701
Db 447 VPIVPSQOAKPLKDRSAEET 468

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RESULT 12  
T13960  
beige protein homolog - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C:Accession: T13960  
R:Mori, M.; Nishikawa, T.; Higuchi, K.; Nishimura, M.  
submitted to the EMBL Data Library, November 1998  
A:Description: Deletion in the beige gene of the beige rat due to recombination between  
A:Reference number: Z17837  
A:Accession: T13960  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA

A:Accession: T42730  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-3788 <OR>  
A:Cross-references: EMBL:AB020019; NID:d1241953; PID:BAA34688.1  
A:Experimental source: strain DA; spleen  
C:Genetics:  
A:Gene: beige

Query Match 2.74; Score 108.5; DB 2; Length 3788;  
Best Local Similarity 19.4%; Pred. No. 31;  
Matches 144; Conservative 98; Mismatches 267; Indels 235; Gaps 38;

QY 20 GSOLAVAGSGRGADTCGWRKAAARPLCVANEGVPASRNSGLNYITEVDNCTT 79  
DB 651 GETLOGTLCAGSGCLSPSYRF-----QGILP---SSGSEDLKWDALDA 695  
QY 80 YLNPVGHVADQNTTISQVACH--DOVAVTILMSPGAGIEFLKGRFVILEELKSEG- 136  
DB 696 YONFIPOE--DRLHNTQASHICNLQKGNVIVQW-----KLYNIENFVLQGV 743  
QY 137 ---ROCQOLTKDPKQLNSSFRTGMSOPFLNKKET-DYFVKVVP-----EP 181  
DB 744 ELVHCQQLSI-----TSNTHMSQLKQVLPQEVLYLKLPLILLKSRVIRDLFL 795  
QY 182 SIKN-----ESNY---HFF-FFTRACDILLQDNLACKFFKPRNLMISQSDMQ 229  
DB 796 SCGNVHIETLNYLOGIRSHSLKAFETLIVSLAGEQOKRAAVPGV---DGLDIOQELSL 852  
QY 230 VSPDHAPHNFGFFVLYKHKHGPFRKTKQEQTTTSCLLQNVSPGDYIIELVDD 289  
DB 853 V-----GPSLHK-----QOASTDSCSLRK-----EYASLRDT 880  
QY 290 TNRTRKVMYALKPVSHPAGPIRAVAITVPLVVISAFATLVTCRKKQENIYSHLDE 349  
DB 881 DPKRKTVHO-----DAHINTINFLCVAF-----LCVSKZADSRESAN- 920  
QY 350 ESSESSTY---TAALPRERLRPRKVFVLCYSKQDNHNVV---QCFAYLQDFCGCEV 403  
DB 921 ESDTGYDSTASEPLSHMLPRLS-----ENVLPSPCELLH-----958  
QY 404 ALDWEDESLCHGQRENV---LOKHESQFI---IVVCSKMKYFVDKKNYKKGGRG 457  
DB 959 ADLW---SNCR---NIYMLNSVFOFHRGGFQVCHL-LIFMIOKLFKRSHTEDQG 1009  
QY 458 SGKGEFLF-----LVASAIAEKLRQAKQSSAALSFKFIAYFYDYSCEGDPGILD- 507  
DB 1010 RROGEMSVNKGKGLARISOPENMILKEDVSSSTAPEPGFLKSGADRVSLESHLPTSAE 1069  
QY 508 --LSTR-----YRLMDNLPOLCSH---LHSDRGLOEPGQHTROG 542  
DB 1070 QILATKSIPGEAKTFMNOESTCLOSLIRLESLLAICLSASQOKMELELPQO----- 1124  
QY 543 SRNRYFRSGSLVAVICNHQFIDEP-----DMFEKQFVFPFPPPLRYREP 591  
DB 1125 -----SLSLENILCELRHLSQKVAETELAKPLFDALLVALGNISADLDPGDT 1174  
QY 592 VLEKFDGSLVLDVCKPESDFCLKVEAVILGATG---PADSQHESQHGGLDQDGE 646  
DB 1175 VTEKSHPS---BEVLSQDFSEAEADSQCCLSLKLGEEGYEADSNESPEGETQDDGV 1231  
QY 647 ARPALDG--SNAALOP--LLHTVAKG 667  
DB 1232 ELPEAGFGSGSIVPNMLLESTHG 1255

RESULT 13

Bassoon protein - mouse  
T42730  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T42730  
R:Dieck, S.; Sammarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998  
A:Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized  
A:Reference number: 222249; MUID:98345363; PMID:9679147

A:Accession: T42730  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-3942 <DIE>  
A:Cross-references: EMBL:Y17034; NID:g3413809; PIDN:CAA76598.1; PID:g3413810  
A:Experimental source: strain 129 SVJ  
C:Genetics:  
A:Map position: 9P1  
A:Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1  
C:Function:  
A:Note: bassoon  
A:Description: may be involved in cytomatrix organization at the site of neurotransmission  
A:Note: component of the presynaptic cytoskeleton  
C:Keywords: coiled coil; zinc finger

Query Match 2.74; Score 107.5; DB 2; Length 3942;  
Best Local Similarity 19.1%; Pred. No. 39;  
Matches 58; Conservative 29; Mismatches 99; Indels 117; Gaps 11;

QY 516 DNLPCSLHSHROGLQERQHTROGSRNRYFRSKSGSLVAIC-----NMHOFIDEE 570  
DB 3535 DTCOFCS-----SHSPDQVQERVKDGPRAHAYKREBYMLDDSHCVVSDSEAYHLQOE 3589  
QY 571 DMFEKQFVFPFPPPLRYRE-----PVLEKF-----DSGLVLDNDVCKPG 610  
DB 3590 TDMFK-----PRDARSDFRHHGGHTVSSQKRGPARHSYHDYDEPPEGLPHD---EGG 3643  
QY 611 PESDFCLKVEAVILGATGPADSOHESQHG-----GLDQDG-----EAPR- 649  
DB 3644 PGRH-----TSKAEHRHSDHGRHSGRAGEPGRRAKPHARDMGHEARPH 3691  
QY 650 -----ALDGSAAQLPLHTV 664  
DB 3692 PQASPAAPMOKGQPGVPSSADYSQSSRAPSAHYHASESKKSGRAQHTGPSALOPKADTQ 3751  
QY 665 KAGSPDMPRDSGYDVSVPSSLSLPLMEGLSTQDTETSSITSVSSSSGLGEEPPAL 724  
DB 3752 AQPMQGRQAAPGQSQOPPSSROT---PSGTASRQPTQCCQCCQCCQCCQCCQCCQCCQ 3808  
QY 725 PSK 727  
DB 3809 PSQ 3811

RESULT 14

T30851  
lysosomal trafficking regulator, long splice form - mouse  
N:Alternate names: beige protein homolog  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 24-Nov-1999  
C:Accession: T30851  
R:Barbosa, M.D.F.S.; Tchérnev, V.T.; Kingsmore, S.F.  
submitted to the EMBL Data Library, September 1996  
A:Description: Two bg or not two bg? Longest isoform of mouse Lyst (beige) gene.  
A:Reference number: 220903  
A:Accession: T30851  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-3788 <DAR>  
A:Cross-references: EMBL:U70015; NID:g1813541; PID:g1813542; PIDN:AAC53011.1  
A:Experimental source: strain C57BL/6J  
C:Genetics:  
A:Gene: Lyst  
A:Map position: 1  
C:Keywords: alternative splicing

Query Match 2.74; Score 107; DB 2; Length 3788;  
Best Local Similarity 19.5%; Pred. No. 40;  
Matches 156; Conservative 104; Mismatches 288; Indels 254; Gaps 44;

QY 20 GSOLAVAGSGRGADTCGWRKAAARPLCVANEGVPASRNSGLNYITEVDNCTT 79  
DB 651 GETLOGTLCAGSGCLSPSYRF-----QGILP---SSGSEDLKWDALDA 695





GenCore version 5.1.4.p5.4578  
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OK protein - protein search, using sw model

Run on: May 6, 2003, 13:34:41; Search time 14 seconds  
(without alignments)  
2230.834 Million cell updates/sec

Title: US-09-912-157-2  
Perfect score: 4013  
Sequence: 1 MAPWLQCSVFFTVNACLNG.....CQADLGCRSYTDELHVAFL-753

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	310	7.7	866	1 IL17R_HUMAN	Q96F46 homo sapien
2	306	7.6	864	1 IL17R_MOUSE	Q60943 mus musculus
3	135.5	3.4	502	1 IL17S_HUMAN	Q9NM66 homo sapien
4	126.5	3.2	718	1 ISO2_CAEEL	Q10128 caenorhabdi
5	115	2.9	998	1 EPB3_HUMAN	P54753 homo sapien
6	110.5	2.8	499	1 IL17S_MOUSE	Q911p3 mus musculus
7	110	2.7	592	1 STB3_MOUSE	Q60770 mus musculus
8	104	2.6	1462	1 PTP6_DROME	P16620 drosophila
9	103.5	2.6	663	1 RGP2_HUMAN	P47736 homo sapien
10	102	2.5	859	1 ABR2_HUMAN	Q12979 homo sapien
11	101	2.5	1275	1 GRP2_HUMAN	Q13972 homo sapien
12	100.5	2.5	974	1 RHG6_HUMAN	Q43182 homo sapien
13	99.5	2.5	784	1 ZFY2_MOUSE	Q60821 mus musculus
14	99	2.5	783	1 ZFY2_MOUSE	P20662 mus musculus
15	99	2.5	970	1 PSU1_YEAST	P53550 saccharomyc
16	98.5	2.5	993	1 EPB3_MOUSE	P54754 mus musculus
17	98.5	2.5	1050	1 EX5B_CHLPN	Q92797 chlamydia p
18	98	2.4	820	1 CTNB2_TRIGR	P35223 tripneustes
19	97.5	2.4	1845	1 Z236_HUMAN	Q9U136 homo sapien
20	97	2.4	984	1 EPB1_CHICK	Q07494 gallus gall
21	97	2.4	984	1 EPB1_RAT	P09759 rattus norv
22	96.5	2.4	746	1 ABL_MLXVAB	P00521 abelson mur
23	96.5	2.4	902	1 EPBB_XENLA	Q91736 xenopus lae
24	96	2.4	424	1 MK09_HUMAN	P45984 homo sapien
25	96	2.4	660	1 HT31_ARATH	Q04996 arabidopsis
26	96	2.4	1114	1 E2K3_MOUSE	Q922b5 mus musculus
27	95	2.4	828	1 CAN_DROME	Q11002 drosophila
28	95	2.4	933	1 PRGR_HUMAN	P06401 homo sapien
29	95	2.4	1036	1 AXO1_CHICK	P28685 gallus gall
30	94.5	2.4	351	1 HM14_CAEEL	P20271 caenorhabdi
31	94.5	2.4	770	1 GIT1_RAT	Q92272 rattus norv
32	94.5	2.4	841	1 IE63_MCAYS	Q69154 murine cyto
33	94.5	2.4	1011	1 M3K6_HUMAN	O95382 homo sapien

34	94	2.3	984	1 EPB1_HUMAN	P54762 homo sapien
35	94	2.3	2044	1 SIF2_DROME	P91620 drosophila
36	94	2.3	2064	1 SIF1_DROME	P91621 drosophila
37	94	2.3	3224	1 RBP2_HUMAN	P49792 homo sapien
38	93.5	2.3	806	1 RMIL_CHICK	Q04982 gallus gall
39	93.5	2.3	807	1 RMIL_COTJA	P34908 coturnix co
40	93.5	2.3	901	1 A180_MOUSE	Q61548 mus musculus
41	93.5	2.3	915	1 A180_RAT	Q05140 rattus norv
42	93	2.3	429	1 EPC_RAT	P01855 rattus norv
43	92.5	2.3	347	1 SH33_MOUSE	Q62421 mus musculus
44	92.5	2.3	548	1 IDO_MOUSE	P98154 mus musculus
45	92.5	2.3	684	1 FBUL_CHICK	O73775 gallus gall

#### ALIGNMENTS

RESULT 1  
IL17R\_HUMAN  
ID IL17R\_HUMAN STANDARD; PRT; 866 AA.  
AC Q96F46; Q43844;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DE Interleukin-17 receptor precursor (IL-17 receptor).  
IL17R.  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=T-cell;  
RA YAO Z., SPRIGGS M.K., DERRY J.M.J., STROCKBINE L., PARK L.S.,  
RA VANDENBOS T., ZAPPONE J., PALINTER S.L., ARMITAGE R.J.;  
RT "Molecular characterization of the human Interleukin (IL)-17  
receptor".  
RL Cytokine 9:794-800(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Uterus;  
RA STRAUSBERG R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
-1- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,  
suggesting that additional components are involved in IL17-induced  
signaling.  
-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
-1- TISSUE SPECIFICITY: Widely expressed.  
-1- PTM: Glycosylated.

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EMBL; U58917; AAB99730.1;  
EMBL; BC011624; AAH11624.1;  
Gene; HGNC:5985; IL17R.  
MIM; 605461;  
Receptor; Transmembrane; Signal; Glycoprotein.  
FT SIGNAL 1 31 POTENTIAL  
FT CHAIN 32 866 INTERLEUKIN-17 RECEPTOR.  
FT DOMAIN 32 320 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 321 341 POTENTIAL.  
FT DOMAIN 342 866 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 810 818 POLY-GLU.  
FT CARBOHYD 49 49 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 54 54 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 206 206 N-LINKED (GLCNAC... ) (POTENTIAL).

FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 367 367 V -> A (IN REF. 1).  
 FT CONFLICT 580 580 H -> R (IN REF. 1).  
 SQ SEQUENCE 866 AA; 96131 MW; 28330BED2303B0C9 CRC64;

Query Match 7.7%; Score 310; DB 1; Length 866;  
 Best Local Similarity 23.1%; Pred. No. 5.4e-16;  
 Matches 176; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITEKYDNC--TTLNPNVGRVIAQAQNT-----ISOYACHDQ-----VAVTILMS 113  
 DB 49 NCTVKNSTCLDSDWIHP-----RMLTSPSPKDIQIEHFAHTQOGLFFVAHIEMT 99  
 QY 114 -PGALGIEFLKGRFVILELSEKSGROCOOLLILKDPKLNASKKRTGMSOPFLNKKFTED 172  
 DB 100 LQTDASILYLEGAEISVGLQNTNERLCVR--FEELSKLRHHRRWRFTSFHV-VDPDQE 156  
 QY 173 YFVKV--VPPSINKESNTHPFFTRACDLLOPDNLACK---PMPKPRNL-----219  
 DB 157 YEVTVHLPRPIPDGDPNEQSKNFLVPCDEHARKMVTTPCMSSGSLMDP-NITVETLEAH 215  
 QY 220 -----NISGSDMOVSFDAPHNGRFFRYLHYKLHKGEPKRTCKOQOFTYTT 270  
 DB 216 QLRVSFTLNWSTHYOILTSPHMHNSCFEEMH-HIPAPPEEHOHSNVTTLNLNK 274  
 QY 271 SCILQVSPGDYIIEUVDOT---NTRKVMHYALKPVHSGWAPIRAVAITVPLVLSAF 327  
 DB 275 GCCHQVQIOPFFSSCLNDLHRSATVSCPEMPDTPEDIPYMPLWVFWITGISILLVG 334  
 QY 328 ATLETVNCRKQOENYSHLDESESTYTAALPRERLRPR---KVELCYSSKDGON 383  
 DB 335 SVILLIIVCMTRLRAGRS---EKYSDDTKYDGLPVADLIPPLPRKRWIYISA-DHPL 390  
 QY 384 EMNVQCFAYELQDCGEVALDLWEDESLRCQRETV-----IOKIHESOFIIVCSKG 439  
 DB 391 YVDVLKFAQFLTAGTEVALDLLEQALSEAGVMTWVGROKQEVESNKKIIVLCRG 450  
 QY 440 MYFVDKNNKHKGG-----RGSGKGEFLFVAISAIAEKLROAKQSSAALSRIA 491  
 DB 451 TR-----AKWQALIGRGAVPRLCRGKPVGDLETAAMNMLPDFKR-----PACFGTYVV 501  
 QY 492 VIF-DYSCSDVPGLDSTVRLMDNLPLCLSHLSRDHGLQEPQOHTROG---SRNYP 548  
 DB 502 CYSEVSCDGVDFLGAAPYPLMDRFEV--YFRIQLEMFQGRMHRVGLSGDNYL 559  
 QY 549 RSKSGSLVAICNMHQFIDEEPOTFE-----KQYFFHPPLRYREPVLKFDOSGL 600  
 DB 560 RSPGRLRAALDRFRDQVHCPCDWFCEENLYSADQDAPSLDEEV-FEELPLP-GTGI 617  
 QY 601 VLANDVCKPGPESDFCLVEAALVAGTAPADSQHE-----SOHGG 640  
 DB 618 VKRAPLVRE-PSQACLAIDPLVGEEGAATAVAKLEPLHQRPQAPQAPLHLVLAEEGA 676  
 QY 641 LDQDGEAPALDGS--ALO-----PLHTVKAGSPMDPRDGGIYDSSVPSSELSLP 691  
 DB 677 LVAAPVGLDGAVALRALAGEACPLLGSPGAG-----RNSVLF---LPVDPBDS 727  
 QY 692 LMBGLSTDOTETSSLTSSVSSSGLGEPEPPALPSKLLSGSGCKRADLGC 740  
 DB 728 L--GSSTPNASPDLLPEDVR-----EHLGLMLSLFEQSLSCQAQGC 768

## RESULT 2

117R\_MOUSE  
 ID 117R\_MOUSE STANDARD; PR; 864 AA.  
 AC Q60943;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-17 receptor precursor (IL-17 receptor).  
 GN IL17R.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC1 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC1 NCBI\_TaxID-10090;  
 RN (1);  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=thymic lymphoma;  
 RX MEDLINE=96111968; PubMed=8777726;  
 RA Yao Z., Fanslow W.C., Seldin M.F., Rousseau A.M., Painter S.L.,  
 RA Comeau M.R., Cohen J.I., Spriggs M.K.;  
 RT "Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a  
 RT novel cytokine receptor.";  
 RL Immunity 3:811-821(1995).  
 CC 1--FUNCTION: Receptor for IL17. Binds its ligand with low affinity,  
 CC suggesting that additional components are involved in IL17-induced  
 CC signaling (By similarity).  
 CC 1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; U31993; AAC52357.1;  
 DR MGD; MGI:107399; IL17r.  
 DR Receptor; Transmembrane; Signal; Glycoprotein.  
 KW SIGNAL 1 31 POTENTIAL.  
 FT CHAIN 32 864 INTERLEUKIN-17 RECEPTOR.  
 FT DOMAIN 32 322 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 323 343 POTENTIAL.  
 FT DOMAIN 344 864 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 809 814 POLY-GLU.  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;

Query Match 7.6%; Score 306; DB 1; Length 864;  
 Best Local Similarity 22.5%; Pred. No. 1.1e-15;  
 Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

QY 40 GWRM-----KAAAPRL-----CVANEGVGPASRNSGLYNITFYDCTTLYNPVK 86  
 DB 17 GWILLLLNVLAPGRASPLLDFFAPVCAQEGLSGCRVKNSTCLDSDSWHKNLTSPSKNI 76  
 QY 87 HVIADAQNTISQYACHQVAVT-ILWS-PGALGIEFLKGRFVILELSEKSGROCOQ-----141  
 DB 77 YI-----NLSVSTQHGELVPVLRVEMTLQTDASILYLEGAEISVGLQNTNERLCVKFO 131  
 QY 142 --LILKDRQLNSFKRTGMSOPFLNKKFTEDYFVKVPPSPKSNYHPFFETRAC 199  
 DB 132 LSLMLQHRKRNRESF-----SHFVVDPCQEVETVHLPRKIPDGPDKHKSIIIPVDC 185  
 QY 200 D-----LLLQPDNLACKPWPKNLNI-----SQH-----GSDAQV 230  
 DB 186 EDKMKMTTSCVSSGSLMDP-NITVETLQTLRVDFTLHNESTPYOVLESFSDSEHS 244  
 QY 231 SFD-----HAPNFGFRFFLYHYKLKHE---GPKRRTCKOQOFTTSCLL 274  
 DB 245 CFDVVKQIFAPRQEEFHQRANVTFTLSKFKHCCHHVQVQPF-FSSCLND-----CLR 296  
 QY 275 QNVSPGDVILVDDTNTTRKVMHYALKPV--HSP-WA-GPIRAVAVTVPLVVISAFATL 330  
 DB 297 HAVTVPCPVI-----SNT-----VPRPVADYIPLWYGLTITLAI-----LLVGSVIL 341  
 QY 331 FTVMCRKKQENIYSHLDESESTYTAALPRERLRPRKRVFLCYSSKDGONHNMVQC 390

Db 342 IICMRLSGADQKEGDSKINGILVADLTTPPLPR-KVIVISA-DHPLYVEVLK 399  
 QY 391 EYFLODCCGEVALDNEFSLCQREWIQK---IHESOFIVCSGKMYFVDK 446  
 Db 400 FQFLITACGVEVALDLEQVISEVGVNTWVSRKQEMVESKILILCSRG---TQ 454  
 QY 447 KNYREKGG---GRSGKGELFLVAVSAIAEKLROAKOSSAALSFKFIAYFDY 496  
 Db 455 AKWAILGAWPAVOLRCBHWKPGAGDLTAAMNMLDPFR---PACFGYVVCYFSG 509  
 QY 497 SC-EGDVPGLDSTKYLMDNLPCLSHLRSRQGLQECQ---HFGQSRNYSRSKSG 553  
 Db 510 ICSRDVDPNITSRIPLMDREEV---YFRIQDLEMFGRMHVRLTGNTLQSPSG 567  
 QY 554 RSLVAINCHHOIFIDEEDWFKQFYFPH---PPLR---YREPVLEKFDGSLVNDYM 606  
 Db 568 ROLKAVLRFOEMOTQCPDWERENICLADQDLPSLDEEVEDPLPP-GGIVKQOPL 626  
 QY 607 CRPGESDCLKVAIVGATGADSOHSGHGLDQD---GEAR 648  
 Db 627 VRELPSDGLVVDVCV---SEESRMALDPLQAPRELVAHTLQSNVLPAGOV 677  
 QY 649 PALDGSAAQPLHTYKAGSDMP---RDS---GIYSSV---PSSLSLPL----- 692  
 Db 678 PA---ARVVEPLHFDGSGAALPMTEDSEACPLLYGQRNSILCLPVDSDDLPLCSTPM 734  
 QY 693 ---MEGLSDYDTETSSITSSVSSSGLGEPEPALPSKILLSGSKADLCGRSYTDE 746  
 Db 735 MSPDHQDAREQLESIMLSVQSLSGPLESNR-PEVLE-----GCTPSEER 784

RESULT 3

117S-HUMAN  
 ID 117S-HUMAN STANDARD; PRT: 502 AA.  
 AC Q9NRM6; Q9NRM6; Q9NRM6; Q9NRM6;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Interleukin-17B receptor precursor (IL-17B receptor) (IL-17 receptor homolog 1) (IL-17R1) (IL17RH1) (Cytokine receptor CRL4).  
 GN IL17B-OR-EV127.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI-TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RA Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G., Shalhoub J.D. Jt.;  
 RT "Ev127 encodes a novel membrane protein with homology to the IL17 receptor."  
 RL Oncogene 19:2098-2109(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF N-TERMINUS.  
 RC TISSUE=Lung;  
 RX MEDLINE=20317118; PubMed=10749887;  
 RA Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J., Barber M.C., Wang M., Wathen K., Hodge V., Fisher C.L., Olsen H., Ruben S.M., Knyazev I., Cho Y.H., Rao V., Wilkinson K.A., Carrell J.A., Ebner R.;  
 RT "A novel cytokine receptor-ligand pair. Identification, molecular characterization, and in vivo immunomodulatory activity."  
 RL J. Biol. Chem. 275:19167-19176(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Zhang W., Cao X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Cervix;  
 RA Strausberg R.;

Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 (5)  
 RN FUNCTION  
 RP PubMed=11058597;  
 RA Lee J., Ho W.H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S., Goddard A.D., Yasura D.G., Vandlen R.D., Wood W.I., Gurney A.L.;  
 RT "IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog IL-17RH1."  
 RL J. Biol. Chem. 276:1660-1664(2001).  
 CC -1- FUNCTION: Receptor for the proinflammatory cytokines IL17B and IL17E. May play a role in controlling the growth and/or differentiation of hematopoietic cells.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); Secreted (isoform 2).  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here), and 2; are produced by alternative splicing.  
 CC -1- TISSUE-SPECIFICITY: Expressed in several endocrine tissues, mostly in fetal and adult liver, kidney, pancreas, testis, colon, brain and small intestine; not detected in peripheral blood leukocytes, lymphoid organs, and most cell lines.  
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 CC EMBL: AF208110; AAF86051.1;  
 DR EMBL: AF208111; AAF86052.1;  
 DR EMBL: AF212365; AAF87876.1;  
 DR EMBL: AF250309; AAK37428.1;  
 DR EMBL: BC000980; AAH00980.1;  
 DR Genev; HGNC:18015; IL17BR.  
 DR MIN; 605458;  
 KW Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.  
 FT SIGNAL 1 17  
 FT CHAIN 18 502 INTERLEUKIN-17B RECEPTOR.  
 FT DOMAIN 18 292 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 293 313 POTENTIAL.  
 FT DOMAIN 314 502 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 67 67 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 103 103 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 197 197 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 283 283 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT VARSPLIC 250 288 LTPYFPTGSGDCIRHKGTVVLCPTQGVFPFLDNKSRPG  
 FT -> VKFSELLWGGKHRLFHSLLRSLLSNALLPADT  
 FT S (IN ISOFORM 2).  
 FT VARSPLIC 289 502 MISSING (IN ISOFORM 2).  
 FT CONFLICT 6 6 L-> I (IN REF. 1).  
 FT CONFLICT 422 426 LFPLA -> SSPCL (IN REF. 2).  
 FT CONFLICT 427 502 MISSING (IN REF. 2).  
 FT CONFLICT 468 468 L -> F (IN REF. 1).  
 SQ SEQUENCE 502 AA; 55884 MW; CDB87586FAAE49CC CRC64;  
 Query Match 3.4%; Score 135.5; DB 1; Length 502;  
 Best Local Similarity 20.1%; Pred. No. 0.0078;  
 Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps 14;

QY 218 NLNISQHSQDMQVSF-----DHAPHNFGFFHYLHYKLKHEGFPKRYTC----- 261  
 Db 143 NANNEDGSPSNVNFSPGCLDH-----IMKYK-----KKCVKAGSLWDPN 183  
 QY 262 -----KOEOTE---TTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKEVHSNAGPIR 313  
 Db 184 ITACKKEETVEVNFYITEL-----GNRYMALIQNSTI-----IGFSQVEPHEKQKT 231  
 QY 314 AVAITVPLWISAFATL-----FTVMCKKQOENIYSHLDESSSS 355  
 Db 232 RASVIVPTVGDSEGATVOLTVPFPTGSGDCIRHKGTVVLC---PQTGVFPFLDNKSRPG 288

QY 356 TYAAL-----PRERL-----PRKVFICYSSKDGQNMN 386  
 Db 289 GMLPLLLSLVATVWVAGYILWVHERIKKTSFTTLLPPIKLVVYSPICEPH-- 346  
 QY 387 VVOCFAYFQDFCGCEVALDWEFSICREGOREWIOKIHESQFLIVCCKGMYEVOK 446  
 Db 347 TICYTFEFLONCRSEVILEWOKKIAENGPMVOMLATOKRAKRVFLLSNVNSVCOG 406  
 QY 447 ANKHGGGSGGKGLFVAVSAIAEKLRQAKSSAALSKFIAYFYDSCGDVPGIL 506  
 Db 407 TCGKSGSPSENQ-DLPLAFNLCSDLR-----SQHLKHYVVVYFREDTKDYNAL 460  
 QY 507 DLSTKYLKMDNLPOLCSHL 525  
 Db 461 SVCPKYLKMDNLPOLCSHL 479

## RESULT 4

YSO2\_CABEL STANDARD; PRT; 718 AA.  
 AC Q10128;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DE Hypothetical 81.6 kDa protein F56D1.2 in chromosome II precursor.  
 GN F56D1.2  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Chordata; Chromadorea; Rhabditida; Rhabditoides;  
 OC Rhabditidae; Pelodidae; Caenorhabditis.  
 OX NCBI\_TaxID=6229;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Chisoe S., Wilson R.;  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
 CC  
 CC EMBL; 039997; AAA81100.1;  
 CC WormPep; F56D1.2; CE01970.  
 KW Hypothetical protein; Transmembrane; Signal.  
 FT SIGNAL 1 30 POTENTIAL.  
 FT CHAIN 31 718 HYPOTHETICAL PROTEIN F56D1.2.  
 FT TRANSMEM 373 393 POTENTIAL.  
 SQ SEQUENCE 718 AA; 81622 MW; 42B9E056288417AA CRC64;

Query Match. 3.2%; Score 126.5; DB 1; Length 718;  
 Best Local Similarity 21.1%; Pred. No. 0.064;  
 Matches 82; Conservative 64; Mismatches 149; Indels 94; Gaps 19;

QY 363 RRLRLRPP-----KVELCYSSKDGQNMNVVQCFAYFLQDFCGCEVALDWEFDS 412  
 Db 398 RDKVRSREVRNIALTEFKVMIVYAD-DNDLHDCVKLVENLNCASCDVPDFDKLIT 456  
 QY 413 LCREGOREWIOKIHESQFLIVCCKGMYFVDDKNYKHGGSGKGEFLVAVSATA 472  
 Db 457 AQIVPSRWLVQVLSLKKLIIVVSDCAEKILDTASTHOLVORFALDGFAPNEMI-- 515  
 QY 473 EKLRAKQSSAALSKFIAYFYDSCGDV-----GILDSTKYLKMDNLPOLCSHLHSRD 529  
 Db 516 --IRDATNFPEARKYAVFRNYS--PHVPPNLAFLNLT-FTLPQFAQLTAFLHNVE 570  
 QY 530 HGLQFPQGTGROGRRNRYFSKGRSLY---VAICNHOEIDEEPDMFEKQFV----- 580  
 Db 571 H-----TERANTVONISEAQIHENNICASRMMSFFVRPNWLETRWPKDELAA 619

QY 581 FHPPPLRYREPVLKFDGLVNDVMCKPGPSDFCLKVEAAVLGATGPADSQHSGG 640  
 Db 620 LH--LKQSPVIVPIQT-----EED---RIAASIKINLVPPQALVDS-- 657  
 QY 641 LDQGEARPDGSAALQPLHETVKAGSPDM-PRDSGYDSSVSSLSLPLMEGLST 698  
 Db 658 -DED-----DVDLQP--HASHQNPQLILLPPEQCG-----PDS--SD 690  
 QY 699 DOTETSLTESVSSSGLGEEPPALPSK 727  
 Db 691 SEDSSSESESDNEG---EDPKTIYVK 716

## RESULT 5

EPB3\_HUMAN STANDARD; PRT; 998 AA.  
 AC P54753;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ephrin type-B receptor 3 precursor (BC.2.7.1.112) (Tyrosine-protein  
 DE kinase receptor HEK-2).  
 GN EPB3 OR ETK2 OR HEK2.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=93390963; PubMed=8397371;  
 RA Boehme B., Holtrich U., Wolf G., Luzius H., Grzeschik K.-H.,  
 RA Streibhardt K., Ruebsamen-Waigmann H.;  
 RT PCR mediated detection of a new human receptor-tyrosine-kinase, HEK  
 RT 2.  
 RL Oncogene 8:2857-2862(1993).  
 CC -FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO  
 CC EPHRIN-B1 AND -B2.  
 CC -CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein  
 CC tyrosine phosphate.  
 CC -SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -TISSUE SPECIFICITY: UBQUITOUS.  
 CC -SIMILARITY: CONTAINS 1 SAM DOMAIN.  
 CC -SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))

CC EMBL; X75208; CAA53021.1;  
 CC HSSP; P28323; I84F.  
 CC Genew; HGNC:3394; EPB3.  
 CC MIM; 601839;  
 DR InterPro; IPR001090; Ephrin\_receptor.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003962; FNIII\_repeat.  
 DR InterPro; IPR001660; SAM.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR001436; YKase\_receptor.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR Pfam; PF01404; EPH\_lbd; 1.  
 DR PRINTS; PR00014; FNTPEIII.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Euk\_pkinase; 1.

DR PRODOM: PD001495; Ephrin\_receptor; 1  
 DR SMART: SMO0060; FN3; 2  
 DR SMART: SMO0454; SM; 1  
 DR PROSITE: PS00219; TYR\_KIN\_V\_1; 1  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1  
 DR PROSITE: PS00101; PROTEIN\_KINASE\_DOM; 1  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1  
 DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1  
 DR PROSITE: PS00105; SAM\_DOMAIN; 1  
 KW transferase; tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 KW SIGNAL 1 33  
 FT CHAIN 1 33  
 FT DOMAIN 34 398  
 FT TRANSMEM 34 559  
 FT DOMAIN 560 580  
 FT DOMAIN 581 998  
 FT DOMAIN 199 336  
 FT DOMAIN 337 448  
 FT DOMAIN 449 544  
 FT DOMAIN 633 896  
 FT DOMAIN 935 989  
 FT SITE 936 998  
 FT NP-BIND 639 647  
 FT BINDING 665 665  
 FT ACT\_SITE 758 758  
 FT MOD\_RES 608 608  
 FT MOD\_RES 614 614  
 FT MOD\_RES 792 792  
 FT MOD\_RES 942 942  
 FT CARBOHYD 351 351  
 FT CARBOHYD 445 445  
 SQ SEQUENCE 998 AA; 110286 MW; 57C82C397CC61103 CRC64;  
 Query Match  
 Best Local Similarity 19.09; Pred. No. 0.78;  
 Matches 158; Conservative 122; Mismatches 301; Indels 250; Caps 42;  
 QY 35 GATCGGKRWKAARPLC-----VANEGVGA-----SRNSG-----LYNTFR 73  
 DB 267 GATCATGHEPAKESQCPGPGSYAKAGQEGCLPCPNKRTSPASICTCHNFYR 326  
 QY 74 YDN-----CTYLPVNGKHVIADAQNTISQYACHDQVAVYILRS-FCALGIEFLKGR 126  
 DB 327 ADSDSADSACTVPSP-PRGVISN-----NETSLILESEPRDLGVDRDLLN 374  
 QY 127 VILEELKSG-----ROCOQLIKDPKOLNSFRKGTGMSQPLANKFETDYEVKVVPEP 181  
 DB 375 VICKKCHGAGSACSRCDNVEFPVQLGLSEPRVHTS-----HLAHTRYTEVQAVN 429  
 QY 182 SIKNESNYHFFTRACDLQLQDNILACKPFKPNRLNISQSDMOVSFDHAPHNGF 241  
 DB 430 GVSCKPLPRPRAAVNITNQAAPSEV-----PTLRHSSSGSLTSLNAPPERNG- 481  
 QY 242 RFYLYHKLKHEGP-KKTKCQBOTETTSCLLQWSP-GDYIIELVDDNTTRKVMHY 299  
 DB 482 --VILYEMKY--FEKSEGIATVTSQMSVQLDGLRDARYVQV-----RARTVAGY 531  
 QY 300 A--LKPVH-----SPWAGPIRAVATVPLVVISAFATL-----FTVCKRKKQENIYS 345  
 DB 532 GQYSRAPEFETTSERGAQOLQQLPLVGSATAGLVFAVVVATVCLRKORH----- 587  
 QY 346 HLDSESESTYTAALPRERLRPRKPVFLCYSSKQDNEMVNVQCFAYFLODFC-GCEVA 404  
 DB 588 -----GSDSEYTEKL-QQYIAPGMKYVIDPFTYEDPN--EAVREAKEIDVSCVKEEV 638  
 QY 405 LDWEDFSLCRGQREWIQIHESQFIIVVCSKGMKYFDKNTKHKGGGSGSGKSELF 464  
 DB 639 IGAGEFGEVCR-----GRKQPGREVEF 661  
 QY 465 LVAVSAT-----AEKLROAKQSSAALSFKFIATVFDYSCGDVPGILDLS-----TKYR 513  
 DB 662 -VAIKTLKVGTERQRDRFLSEASIMQGF-----DHPNIIIRLEGVVTTSRPMI 709

QY 514 ---LMDNLPCLSHLHSDRGLEPGQHT-----ROGSRNRY-FRKSQGR 554  
 DB 710 LTFEMENC-ALDSFRLND-----QFTVIQVGLMGLGIAAGMKYLSERNYVHROLAAR 762  
 QY 555 SIKV---AIC-----NMHQFIDEEDPFQKVPFHP-----PLRYREP---VLEKED 597  
 DB 763 NILVANSNLVCKVSQFGLSRELEDDPS-----DPTTSSLAGKIPIRWTAPEAIAYRKEF 816  
 QY 598 S-----GLVNDVMCKKCPESDFCLKVEAAVIGATGPADSOHESQHGGLDODGEARPA 650  
 DB 817 SASDWSVSGIVNVEVMS-----YGERPYWMSNQDVINAVEQDYRLPPP 860  
 QY 651 LGSAAQLPLHTVKAQSPDMRDSGIYDS-----SVPSELSLPLMEGL 696  
 DB 861 MOCPTALHQLMDCWVRDRNLRPKFSQIVNTLKLIRNAASLKVINASQSGMSQPLDRT 920  
 QY 697 STDQTSLSLTSVSSSSGLGEEPEPALPSKLLSSGCKADLGRSYTDEL 747  
 DB 921 VPDYTTFTTVGDMLDAIK-MGRYK-----ESFVSAGFASFDLVAQMTAEDL 965

RESULT 6  
 IL17S\_MOUSE STANDARD; PRT; 499 AA.  
 AC Q9JIP3; Q9JIP2;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-17B receptor precursor (IL-17B receptor) (IL-17 receptor homolog 1) (IL-17RH1) (IL17RH1) (IL-17ER).  
 GN IL17B OR EVI27.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=20273223; PubMed=10815801;  
 RA Tian E., Sawyer J.R., Largaespada D.A., Jenkins N.A., Copeland N.G.,  
 RA Shaughnessy J.D. Jr.;  
 RT "Evi27 encodes a novel membrane protein with homology to the IL17 receptor";  
 RL Oncogene 19:2098-2109(2000).  
 CC -1- FUNCTION: Receptor for the proinflammatory cytokines IL17B and IL17E. May play a role in controlling the growth and/or differentiation of hematopoietic cells.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); Secreted (isoform 2).  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Liver and testis. Expressed at lower level in kidney and lung. Expressed in selected T-cell, B-cell and myeloid cell lines.  
 CC -1- MISCELLANEOUS: EVI27 is a common site of retroviral integration in BXH2 murine myeloid leukemias, localized near the IL17B gene. Proviral integrations result in increased expression of IL17B on the cell surface.  
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 CC EMBL; AF208108; AAF86049.1;  
 CC EMBL; AF208109; AAF86050.1;  
 CC MGD; MGI:1355292; Il17br.  
 KW Receptor; Transmembrane; Signal; Glycoprotein; Alternative splicing.  
 FT SIGNAL 1 17  
 FT CHAIN 18 499 INTERLEUKIN-17B RECEPTOR.

FT DOMAIN 18 286 EXTRACELLULAR (POTENTIAL)  
 FT TRANSHEM 287 307 POTENTIAL  
 FT DOMAIN 308 499 CYTOPLASMIC (POTENTIAL)  
 FT CARBOHYD 67 67 N-LINKED (GLNAC) (POTENTIAL)  
 FT CARBOHYD 103 103 N-LINKED (GLNAC) (POTENTIAL)  
 FT CARBOHYD 156 156 N-LINKED (GLNAC) (POTENTIAL)  
 FT CARBOHYD 197 197 N-LINKED (GLNAC) (POTENTIAL)  
 FT VARSPLIC 163 218 LHWYKIKKQCTGSLNDPDIACKKKKVVNFITNPL  
 FT GSKYTIQRTDILG->TRENTEVTSGVPAKHOALRI  
 FT SAPPFLAPFGPDSVILPQPPLASLFDHFKLT (IN  
 FT ISOFORM 2)  
 FT VARSPLIC 219 499 MISSING (IN ISOFORM 2)  
 FT SEQUENCE 499 AA; 55617 MW; C65440430E3C31F3 CRC64;  
 SQ  
 Query Match 2.8%; Score 110.5; DB 1; Length 499;  
 Best Local Similarity 24.1%; Pred. No. 0.66;  
 Matches 40; Conservative 27; Mismatches 82; Indels 17; Gaps 4;  
 QY 355 STYTAALPRELRPRKVFYLCSTSSDGNHNNVQCTAYFLQDFCCGCEVALDWFDFSLC 414  
 DB 314 STKTSFPISTMLPLKLVLPVTPSEICFHH--TVCFRTDFLQNYCSEVILEKWKOKKIA 371  
 QY 415 REGOREWYQIKHESOFIIVVCSKGYFVDKKNYKHGGGSGRGELFLVAVSAIAEK 474  
 DB 372 EMGPVQWLTQKAAQKVVFLPSPVPTLCSACGHNSARENSQ--DLFPLAFLNFCSD 430  
 QY 475 LQAQKSSAALSKEITAVDFYSCGDVPGILDISTYRLMDNLQ 520  
 DB 431 F-----SSQTHLKLIVYL-----GGADLGDYNALSVCPQ 462

RESULT 7  
 STB3\_MOUSE  
 ID STB3\_MOUSE STANDARD; PRT; 592 AA.  
 AC Q60770;  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE SynTaxin binding protein 3 (UNC-18 homolog 3) (UNC-18C) (MUNC-18-3).  
 GN STABP3 OR UNC18C.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-95197608; PubMed-7890715;  
 RA Tellam J.T., McIntosh S., James D.E.;  
 RT "Molecular identification of two novel Munc-18 isoforms expressed in  
 non-neuronal tissues.";  
 RL J. Biol. Chem. 270:5857-5863(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/c; TISSUE-Brain;  
 RX MEDLINE-96421662; PubMed-8824310;  
 RA Gengyo-Ando K., Kitayama H., Mukaida M., Ikawa Y.;  
 RT "A murine neural-specific homolog corrects cholinergic defects in  
 Caenorhabditis elegans unc-18 mutants.";  
 RL J. Neurosci. 16:6695-6702(1996).  
 CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.  
 CC -1- SIMILARITY: BELONGS TO THE STXBP/UNC-18/SEC1 FAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; U19521; AAA69913.1;  
 DR EMBL; D30798; BAA19478.1;  
 DR MGD; MGI:107362; Stxbp3.

DR InterPro; IPR001619; Sec1-like.  
 DR Pfam; PF00995; Sec1; 1.  
 KW Protein transport.  
 SO SEQUENCE 592 AA; 67942 MW; 7874B71DE107871A CRC64;  
 Query Match 2.7%; Score 110; DB 1; Length 592;  
 Best Local Similarity 18.5%; Pred. No. 0.92;  
 Matches 93; Conservative 64; Mismatches 157; Indels 188; Gaps 22;  
 QY 321 LWISAFATLFTVCKKKQKQ-----ENISHLDESSSTYTAALPRELRPRK 371  
 DB 34 IMLDDEFTTKLSSCKMTDLLEGITVNIKNRPVROMKALYF-----ISPTK 86  
 QY 372 VFICYSSKSDGNHNNVQCFAYFLQDFC-----GCE-----402  
 DB 87 SYVCFLEDFGSKSEKKYKANYIYFDPCPSLNFKNKASCSKSIIRCKEINISFPOESQ 146  
 QY 403 VALDLWEDFSLC-----REGOREWYQIKHESOFIIVV-----SKMKY-----442  
 DB 147 VYTLDPDAFYCYSPDSNASRKEVWMEAEQ--IVTVCATLDENPCVRYKSKPLDNA 204  
 QY 443 ----FVDRK--NFK--HKGGRSGRGELFLV-----AVSAIAEKLRQAKQSSAALS 487  
 DB 205 SKLAQLVERKLEDYKIDKGLIKGKTQSOLLIDRGDFDPVSTVLHEL-----252  
 QY 488 KFIATYFD-----YSCGE-DVPGIL-----DLSTYK-----LMDNLPCSLHL 526  
 DB 253 TFQAMAYDILLPIENDTYKYTDGKEKAVLEEDDLWVRVHRHIAVLEGIPLKMEIS 312  
 QY 527 SRDHGLQEPQHTROGSRNRYFRSKRSYVAICNNHOFIDEEPWFKEQVFVPHPPPL 586  
 DB 313 STK-----KATEKTSLSALTOLMEKMPFRKQISKQV-----HL 348  
 QY 587 RYREPVLKFX-----DSGLVLDVNCVCKPGSPESDFCLKVE 620  
 DB 349 NLAEDCNKFKNIERKLECKTQDIALGTADGAGVRKDSMLVLPVLL--NNHNCOKIR 406  
 QY 621 AAVIGATGAPDSOHSGHGLDQDGEARPAIDSAALQPLLHTVKGSPSDMRD-SGIY 679  
 DB 407 AVLLYIFGNGTEEN-----LDRLIHNVKIEDDSOMIRNWSHLG 446  
 QY 680 DSSVSPSELSLPLMEGLSTOOT 701  
 DB 447 VPIVPSQQAQPLKDRSAEET 468

RESULT 8  
 PTP6\_DROME  
 ID PTP6\_DROME STANDARD; PRT; 1462 AA.  
 AC P16620;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein-tyrosine phosphatase DPTP precursor (EC 3.1.3.48) (Protein-  
 tyrosine-phosphatase phosphohydrolase).  
 GN PTP69D OR DPTP.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-90046860; PubMed-2554325;  
 RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
 RT "A family of receptor-linked protein tyrosine phosphatases in humans  
 and Drosophila.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
 CC -1- FUNCTION: IT IS POSSIBLE THAT DPTP IS A CELL ADHESION RECEPTOR.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O -> protein  
 tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
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 CC or [send\\_email\\_to\\_license@sib-sib.ch](mailto:send_email_to_license@sib-sib.ch))

CC EMBL: M27699; AA28842.1;  
 DR PIR: B36182;  
 DR HSP: P18052; LYPO;  
 DR FlyBase: FBgn0014007; Ptp69D;  
 DR InterPro: IPR003961; FN\_III;  
 DR InterPro: IPR003006; Ig\_MHC;  
 DR InterPro: IPR003598; Ig\_C2;  
 DR InterPro: IPR003600; Ig\_Like;  
 DR InterPro: IPR00387; TYR-phosphatase;  
 DR Pfam: PF000242; Tyr\_PP;  
 DR Pfam: PF00041; fn3; 3;  
 DR Pfam: PF00047; Ig; 2;  
 DR Pfam: PF00102; Tyrosinphatase; 2;  
 DR PRINTS: PRO0700; PRTYPHPTASE;  
 DR SMART: SM00060; FN3; 3;  
 DR SMART: SM00410; IG\_Like; 1;  
 DR SMART: SM00408; IGC2; 1;  
 DR SMART: SM00194; PTPC; 2;  
 DR PROSITE: PS00383; TYR-PHOSPHATASE\_1; 2;  
 DR PROSITE: PS00056; TYR-PHOSPHATASE\_2; 2;  
 DR PROSITE: PS00055; TYR-PHOSPHATASE\_PTP; 2;  
 KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
 KW Cell adhesion; Immunoglobulin domain; Repeat.  
 FT SIGNAL 1 23  
 FT CHAIN 24 1462 PROTEIN-TYROSINE PHOSPHATASE DPTP.  
 FT DOMAIN 24 805 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 806 823 POTENTIAL.  
 FT DOMAIN 824 1462 CYTOPLASMIC  
 FT DOMAIN 38 119 IG-LIKE C2-TYPE DOMAIN 1.  
 FT DOMAIN 147 221 IG-LIKE C2-TYPE DOMAIN 2.  
 FT DOMAIN 342 437 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 438 538 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 912 1165 PROTEIN-TYROSINE PHOSPHATASE 1.  
 FT DOMAIN 1208 1459 PROTEIN-TYROSINE PHOSPHATASE 2.  
 FT ACT\_SITE 1097 1097 BY SIMILARITY.  
 FT ACT\_SITE 1391 1391 BY SIMILARITY.  
 FT DISULFID 45 112 POTENTIAL.  
 FT DISULFID 154 214 POTENTIAL.  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 162 162 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 429 429 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 451 451 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 516 516 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 603 603 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 701 701 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 755 755 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT SEQUENCE 1462 AA; 167411 MW; P8091D69E88230EB CRC64;

Query Match

2.6%; Score 104; DB 1; Length 1462;

Best: Local Similarity 20.0%; Pred. No. 9.4;  
 Matches 88; Conservative 53; Mismatches 136; Indels 164; Gaps 23;  
 QY 55 NEGVCPSASR-----NSGLNITEKVD-----NCTYLNPYGVKGVADDA 92  
 DB 259 NDGNDPIQFFITLOEAGTFTTHKDFNGSHSYILDHFKPNTYFLRVKNSIGNG 318  
 QY 93 -----QNITISOVACHDOV-----AVTILWSPGALG-IEFLKGRVILEEL 132  
 DB 319 QPTQPPQGITTLVS---DPFIPKVTGTVASTITIGWNPDPDLIDYIQYELIVSE- 374  
 QY 133 KSEGRCQCOLLKDKPKLNSSFKRTGMSQPPLNKKPDTDFYKVPFSPKSNSTYHPF 192  
 DB 375 --SG-----EVPKVEIAIYQNSRLPIV-----FDKLTATDYE-- 408  
 QY 193 FFRTRACDLLOPDLNACKPFW-----KPRNLNISOH-----GSDMQVSF 232  
 DB 409 -FRVRACSDLTK-----TCGP-WSENYNGTMDGVATKPTNLISQCHDNVTRGSIATNW 462  
 QY 233 DHAPHNFCGRFHYL-----HYKLKHE--GPFPRKTC-- 261  
 DB 463 DVPKTPNGKVVSYLIHLGNPASTVDREMGPKIRRIDEPHKHTLYESVSPNTYTVVS 522  
 QY 262 -----KQQTTFETTSCLLQNVSPGDIIELVDDVNTTRKVMHYALK---PVHSPWAGPIR 313  
 DB 523 AITREKNGEPATGSCILMPVSTPDATGRMTMSKVNLDK---YVLKLYLPKISERNCP- 578  
 QY 314 AVAITPLVWISAFATLFTVNCRRKQOE-----NIYSHLDEES---SESSTYTAALPR 363  
 DB 579 -----CCRYLVLVRINNDKELPOPEKLNIATIQEVHSDNVTRESSAYIAEMIS 626  
 QY 364 ERLRPRKRVFLCYSSKQGNH 384  
 DB 627 SKYF-RPEIFLGAERFSENN 646  
 RESULT 9  
 RGP2\_HUMAN  
 ID RGP2\_HUMAN STANDARD; PRT; 663 AA.  
 AC P47736;  
 DT 01-FEB-1996 (Rel. 33, Created).  
 DT 01-FEB-1996 (Rel. 33, Last sequence update).  
 DT 15-JUN-2002 (Rel. 41, Last annotation update).  
 DE Rapi GTPase activating protein 1 (RapiGAP).  
 GN RAP1GAP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE-91256304; PubMed-1904317;  
 RA Rubinfeld B., Munemitsu S., Clark R., Conroy L., Watt K.,  
 RA Crossier W.J., McCormick F., Polakis P.;  
 RT "Molecular cloning of a GTPase activating protein specific for the  
 RT Krev-1 protein p12rap1".  
 RL Cell 65:1033-1042(1991).  
 RN [2]  
 RP TISSUE SPECIFICITY, AND INDUCTION.  
 RX MEDLINE-98010656; PubMed-9346962;  
 RA Kurachi H., Wada Y., Tsukamoto N., Maeda M., Kubota H., Hattori M.,  
 RA Iwai K., Minato N.;  
 RT "Human SPA-1 product selectively expressed in lymphoid tissues is a  
 RT specific GTPase-activating protein for Rapi and Rap2".  
 RL J. Biol. Chem. 272:28081-28088(1997).  
 CC -1- FUNCTION: GTPase activator for the nuclear ras-related regulatory  
 CC protein RAP-1A (KREV-1), converting it to the putatively inactive  
 CC GDP-bound state.  
 CC -1- SUBCELLULAR LOCATION: Associated with Golgi membranes.  
 CC -1- TISSUE SPECIFICITY: Significant expression seen in the brain,  
 CC kidney and pancreas. Abundant in the cerebral cortex and expressed  
 CC at much lower levels in the spinal cord. Not detected in the

CC lymphoid tissues.  
CC -1- INDUCTION: By 12-O-tetradecanoylphorbol-13-acetate (TPA) in  
CC promyelocytic HL-60 cells.  
CC -1- SIMILARITY: CONTAINS 1 RAP/RAN-GAP DOMAIN.  
CC  
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CC  
CC EMBL: M64788; AAC60252.1;  
CC GenBank: HGNC:9858; RAP1G1.  
CC MIN: 600278;  
CC InterPro: IPR003109; GTPase\_LGN.  
CC InterPro: IPR000331; Rap\_GAP.  
CC Pfam: PF02145; Rap\_GAP; 1.  
CC Pfam: PF02188; Rap\_GAP; 1.  
CC SMART: SM00390; GoLoco; 1.  
CC KW: GTPase activation; Membrane.  
CC FT: DOMAIN 210 397  
CC SEQUENCE 663 AA; 73391 MW; 3703B7CC603404DA CRC64;  
CC  
CC Query Match 2.68; Score:103.5; DB:1; Length 663;  
CC Best Local Similarity 19.58; Pred. No. 3.4;  
CC Matches 143; Conservative 80; Mismatches 262; Indels 247; Gaps 33;  
CC  
QY 167 MKFTDYFVKVFPFSSIKNESNYHFFFRACDLQPD----- 206  
DB 1 LATEEDY-----IPYPSV-----HEVLGREGPPPLILLPOFGYINTEGNIHSIPETE 70  
QY 207 -----NLACKP-----FWKPRNLNISQSGDMQVDFDHPNFGRFFLYHYK 249  
DB 71 PLOSPYTKVLECNPTARYIKHFLGKEHF-----YSLDTA-----LGLHVFSLKYD 119  
QY 250 L-----KHGPFKKTKQKQDTTETSCLLQNVSGDYIELVDDTNTTRKVMHVALKPVH 305  
DB 120 VIGQEHLLRLLTCTRYHDVPIISCLTEFPNVQMAKLVGCEVDNVDR-----FYPLV 173  
QY 306 SPNAGPRAVAITVPLVWIS-----AFATLFTVMCKKQOENIYSHLDESSSESYTAAALP 362  
DB 174 YPRAS-----RLIYTFDEHVISNNFEGYIKLGTSEER-----LFSNEESPAFVEFLE 225  
QY 363 RERLRPRKVFCLYCKSKQGNHNVQCFNFIQDFGCGEVALDWE-----DFSLCR-- 415  
DB 226 -----FLGQKVK-----LQDFKGRGGLDVTHTGQTGTSVYCNFR 260  
QY 416 -----EGQREWIQIHESOFIIVVCCKGMKVFVDK-----KNYK 450  
DB 261 NKEIMPHVSTKPLPYTEGDAQOQLKRRHIGNDIVAV-----VFQDENTPEVPDMIASNFI 314  
QY 451 H-----KGGGSGSGKGELEFVAVSAIAE-----KLQKQKSSAALSXFA 491  
DB 315 HAYYVQAEGG-----PDGLIKVSTVARDVDVFPGLPDPVAFKRGPEFOEFLTKLIN 371  
QY 492 VYFDYSC-EGDVPGLDLSYRLMDNLPLQCLSHLSRD-HGLQBPQGHTRQSGRRNYF- 548  
DB 372 A--EYACYKAERFAKLEERTRAALETLYEEL-HIHSQMWGLGDEKMGSGGGFF 428  
QY 549 -----RSKSGSL-----YVAICNMHQFDDEPDWFE-----KQVPHPPPLR 587  
DB 429 ESFVRVIRSGSDMAGLSNKKNTVSTSHSGSFAPNPDIAKAGLSLIVPKSPTRK 488  
QY 588 YREPVLKEDSLGLVNDYMKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQGEA. 647  
DB 489 KSGPFGSRSSAIGIENI-----QEVQKRESPPAGQKTP-DSGHVSYQPKSE----- 535  
QY 648 RPAIDGSAAOLPLHTVAGSPDMPDRSGIYDSSVPSSELS-----LPLMEGLSTQTE 702  
DB 536 -----NSTGSSPMPETTKNRAETAQRAEALKOFKSRSSSSASSFASVVEETEGVDGDTG 591

QY 703 TSS-----LTSEVSSSSSG-----LGEEPPALPSKL 728  
DB 592 LESVSSSGTPKRSFYITWLEDSVTSITGSGSPSPSPRPDAGKLGDPACPAKEIKQL 651  
QY 729 LSSGSCKADIC 740  
DB 652 EASEQMPQLGC 663  
RESULT 10  
ABR\_HUMAN  
ID ABR\_HUMAN STANDARD; PRT; 859 AA.  
AC Q12979; Q13693; Q13694;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Active breakpoint cluster region-related protein.  
GN ABR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hippocampus;  
RX MEDLINE=94086546; PubMed=8262969;  
RA Tan E.-C., Leung T., Manser E., Lim L.;  
RT "The human active breakpoint cluster region-related gene encodes a  
RT brain protein with homology to guanine nucleotide exchange proteins  
RT and GTPase-activating proteins.";  
RL J. Biol. Chem. 268:27291-27298 (1993).  
RN [2]  
RP SEQUENCE OF 39-859 FROM N.A. (LONG AND SHORT FORMS).  
RC TISSUE=fibroblast; PubMed=8349582;  
RX MEDLINE=93352461; PubMed=8349582;  
RA Heisterkamp N., Kaartinen V., van Soest S., Bokoch G.M., Groffen J.;  
RT "Human ABR encodes a protein with GAPRA activity and homology to the  
RT DBL nucleotide exchange factor domain.";  
RL J. Biol. Chem. 268:16903-16906 (1993).  
RN [3]  
RP SEQUENCE OF 436-597 FROM N.A.  
RX MEDLINE=90067847; PubMed=2587217;  
RA Heisterkamp N., Morris C., Groffen J.;  
RT "ABR, an active BCR-related gene.";  
RL Nucleic Acids Res. 17:8821-8831 (1989).  
CC -1- FUNCTION: GTPASE-ACTIVATING PROTEIN FOR RAC AND CDC42. PROMOTES  
CC THE EXCHANGE OF RAC OR CDC42-BOUND GDP BY GTP, THEREBY ACTIVATING  
CC THEM.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: HIGHLY ENRICHED IN THE BRAIN. MUCH WEAKER  
CC EXPRESSION IN HEART, LUNG AND MUSCLE.  
CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.  
CC -1- SIMILARITY: STRONG, TO HUMAN BCR.  
CC  
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CC  
CC EMBL: U01147; AAC50063.1;  
CC EMBL: L19704; AAC37519.1;  
CC EMBL: L19705; AAC37518.1; ALT\_INIT.  
CC GenBank: HGNC:81; ABR.  
CC MIN: 600365;  
CC InterPro: IPR000008; C2.  
CC InterPro: IPR001331; GDS\_CDC24.



RESULT 11

ID	GNRP_HUMAN	STANDARD;	PRT;	1275_AA.
AC	Q13972			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Guanine nucleotide releasing protein (GNRP) (Ras-specific nucleotide exchange factor CDC25)			
GN	RASGEF1 OR CDC25			
OS	Homo sapiens (Human)			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
CC	NCBI_Taxid:9606;			
CC	[1]			
CC	SEQUENCE FROM N.A.			
CC	MEDLINE-95129875; PubMed-7828890;			
CC	Wei W., Das B., Park W., Broek D.;			
CC	"Cloning and analysis of human cDNAs encoding a 140-kDa brain guanine nucleotide-exchange factor, Cdc25GEF, which regulates the function of Ras."			
CC	Gen. 151:279-284(1994).			
CC	-1- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.			
CC	-1- SIMILARITY: CONTAINS 2 PH DOMAINS.			
CC	-1- SIMILARITY: CONTAINS 1 DBU-HOMOLOG (DH) DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 RAS-GEF DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.			
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CC	EMBL; L26584; AAA58417.1;			
CC	Genew; HGNC:9875; RASGEF1.			
DR	InterPro: IPR001331; GDS_CDC24.			
DR	InterPro: IPR000048; IQ_region.			
DR	InterPro: IPR001849; PH.			
DR	InterPro: IPR000651; RasGEFN.			
DR	InterPro: IPR001895; RasGEF_CDC25.			
DR	InterPro: IPR000219; RhoGEF.			
DR	Pfam; PF00169; PH_2.			
DR	Pfam; PF00612; IQ_1.			
DR	Pfam; PF00617; RasGEF; 1.			
DR	Pfam; PF00618; RhoGEF; 1.			
DR	Pfam; PF00621; RhoGEF; 1.			
DR	SMART; SM00015; IQ_1.			
DR	SMART; SM00233; PH_2.			
DR	SMART; SM00147; RasGEF; 1.			
DR	SMART; SM00229; RasGEFN; 2.			
DR	SMART; SM00325; RhoGEF; 1.			
DR	PROSITE; PS00741; DH_1.			
DR	PROSITE; PS00720; GDS_CDC25; 1.			
DR	PROSITE; PS50096; IQ_1.			
DR	PROSITE; PS50003; PH_DOMAIN; 2.			
KW	Guanine-nucleotide releasing factor; Repeat.			
FT	DOMAIN 22 129			
FT	DOMAIN 204 229			
FT	DOMAIN 240 426			
FT	DOMAIN 467 584			
FT	DOMAIN 1038 1272			
FT	SEQUENCE 1275 AA; 145381 MW; 86C6F5AA1EA451F1 CRC64;			
QY	Query Match	2.5%;	Score 101;	DB 1; Length 1275;
QY	Best Local Similarity	19.2%;	Pred. No. 13;	
QY	Matches	98;	Conservative	66; Mismatches 144; Indels 202; Gaps 24;

116 ALGTEFLKGRF---VILSELASEGQQQL--TLADPKOLNSFFRTCHMESQPLNM-K 168

80 APGVAGKGLKRLVLSGLFSLASEIYINLEALLPKPL---KATATTQPLVLTQQ 135

169 PETDYFVYVFPFSSINYSNHYFFFRTRACDILLQPNLACKPFWKPNLNLISQHSQM 228

136 IETIFY-----KIQDIYIEHKEY-----DNLCPK-----VQGM--DS 166

229 QVSDPHAPHNFG-----FRFFYLHK-----LKHEGPFKRTK 261

167 QVTGHLFQKLSQGLGYKAFVDNKTVAETAKCSQSNQFOKISEELKVKGP--KDS 223

262 KOEOTTETTSCLQNSPGDYIIELVDDTNTKRMVYALKPVHSPWAGP----- 311

224 KOSHTSYTNEALL-----YKPIDRVSTVLVHDLK--HTVPDHPDPLQDLAR 272

312 -----IRAVAITVP-----LVVISAFAT-----LFT--VMCKR 337

273 ISONFLSSINEDIPRTAVTTPKGTETQLVKDGLFVSESSRKLRLHVFETDVLCCAK 332

338 KOENIXSHL-----DEESSESTYTAALPRRLPRPKVFLCYTSSKDG 381

333 LKKTSAKHOQYDCKWYIPLADLVFPSEESAPQVPPDHELEDMMKLSALKSEIQ 392

382 QNHANVQCFAFYLPDQCEVALDLMEDFSLCRGQREWVIOKHESOFIIVCSKMK 441

393 KEKANKGQSHAI-----GKSYLFLLSDYERSEWREAIQKQLQKLAQFVLSVELQVLT 426

442 IYVDKKNYKKGGRSGGKGLFV-----AVSAIAEKLQAKQSSSAALSKEFI 490

427 FRIENRN-----GKSYLFLLSDYERSEWREAIQKQLQKLAQFVLSVELQVLT 476

491 AVIYDSCGDVPGILDLSTKYRLMDNLPCLSHLSDHGLQEPQH-----TROGSR 545

477 GSCFLKTVNIN-----VTSNRDDDSFGLYGLFVIVHSAKGFQKQSANLCTLEVDSP 531

546 NYFRSKSGRLSYLAICNMHQFID-EPDPWFKE 576

532 GYFYSKA-----KTRVFDRTAEPKWDEE 554

Query Match

Best Local Similarity 20.5%; Pred. No. 6.4;

Matches 117; Conservative 57; Mismatches 190; Indels 208; Gaps 25;

116 ALGTEFLKGRF---VILSELASEGQQQL--TLADPKOLNSFFRTCHMESQPLNM-K 168

80 APGVAGKGLKRLVLSGLFSLASEIYINLEALLPKPL---KATATTQPLVLTQQ 135

169 PETDYFVYVFPFSSINYSNHYFFFRTRACDILLQPNLACKPFWKPNLNLISQHSQM 228

136 IETIFY-----KIQDIYIEHKEY-----DNLCPK-----VQGM--DS 166

229 QVSDPHAPHNFG-----FRFFYLHK-----LKHEGPFKRTK 261

167 QVTGHLFQKLSQGLGYKAFVDNKTVAETAKCSQSNQFOKISEELKVKGP--KDS 223

262 KOEOTTETTSCLQNSPGDYIIELVDDT

QY 126 RVILEELSEKROCOQL-ILKD-----PKOLNSFKRQME-----SOPFLMKFETDYFKV 176  
 Db 243 QVFSKMLAEAYVQOQLHVLNPLRPLRMAASCKPPTITDDVSSIFLNS-ETIMELR 300  
 QY 177 VVPFSSIKNESYHPFFERTACDLDLLOPDNLACKPFWKPRNLISO-----HGSDMOVS 231  
 Db 301 QIFYQGLKARISSNPTLVADLDLILP-----MLNIQEFVNRQYSLOI- 346  
 QY 232 FDBAPHNCPREFYHLKHEGPFRRKCKOBQTETTSCLLQNSPGDYIELVD--- 288  
 Db 347 LARCKONRDFKLLKHTEAPD-----C-EERTLETFYPMFQIP-RYILTLHOVLA 397  
 QY 289 ---DNTTKRMVHALKPVHSPWAGPIRAVAITVPLVVISAFATLVCMCRKQOENIYS 345  
 Db 398 HTPHEHVERNSLOYA-----KSKLEELSR 421  
 QY 346 HDESSSESTYTAALPRERLPRKPVFLCYSSKDGQNHMVVOCFAYFLDPCGEVAL 405  
 Db 422 IMHDEVSETEMIRKALERN-----IIE-----GCEILL.451  
 QY 406 DLWEDF-----SLCREGOREVVIQIHESOFIIVVCSKM 440  
 Db 452 DTSQTFVRQSLIOVPMSEKGIKTRGLSLSLEGEROCFLPSKH-----LIICTRGS 506  
 QY 441 --KYFVDKKNY-----KHGGG-----RSGKGELFLVA.467  
 Db 507 GGLHLTKANGVISLIDTLEPEESTEEKANGSGQDIDHDFKIGVEPKDPSPTVILVA 566  
 QY 468 VSAIAELKROAKOSSAALSFKFIATYDYSCGDPVGGILDLSTKYRLMDNLPLCASHLS 527  
 Db 567 SS-----ROEKAATWSDISQVD-----NIRCNGLANNAFENSKV-----TVPMI- 608  
 QY 528 RDBGLQEPQHTROGSRNFRSKSGRSIX 557  
 Db 609 -----KTRGTREAEK-SRSDASLY 628

RESULT 12  
 ID RHG6\_HUMAN  
 AC 043182; 043437; 09P1B3; 09UR81; 09UR82;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Rho-GTPase-activating protein 6 (Rho-type GTPase-activating protein  
 DE RhoGAP2-1)  
 DE RhoGAP2 OR RHOGAP6.  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., REVISIONS, FUNCTION, SUBCELLULAR LOCATION, AND  
 RP ALTERNATIVE SPLICING.  
 RC TISSUE=Fetal kidney.  
 RX MEDLINE=20164286; PubMed=10699171;  
 RA Prakash S.K., Taylor R., Jenna S., Lamarche-Vane N., Armstrong D.L.,  
 RA Xu B., Mancini M.A., Zoghbi H.Y.;  
 RT "Functional analysis of ARHGAP6, a novel GTPase-activating protein for  
 RT RhoA";  
 RL Hum. Mol. Genet. 9:477-488(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=98086484; PubMed=9417914;  
 RA Schaefer L., Prakash S.K., Zoghbi H.Y.;  
 RT "Cloning and characterization of a novel rho-type GTPase-activating  
 RT protein gene (ARHGAP6) from the critical region for microphthalmia  
 RT with linear skin defects";  
 RL Genomics 46:268-277(1997).  
 CC -1- FUNCTION: GTPASE ACTIVATOR FOR THE RHO-TYPE GTPASES BY CONVERTING  
 CC THEM TO AN INACTIVE GDP-BOUND STATE. COULD REGULATE THE  
 CC INTERACTIONS OF SIGNALING MOLECULES WITH THE ACTIN CYTOSKELETON.  
 CC PROMOTES CONTINUOUS ELONGATION OF CYTOPLASMIC PROCESSES DURING

CELL MOTILITY AND SIMULTANEOUS RETRACTION OF THE CELL BODY  
 CHANGING THE CELL MORPHOLOGY.  
 -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: 1, 2, 3 (SHOWN HERE), 4 AND 5;  
 ARE PRODUCED BY ALTERNATIVE SPLICING.  
 -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN KIDNEY, HEART AND SKELETAL  
 MUSCLE FOLLOWED BY RETINA, LYMPHOBLAST, PLACENTA, LUNG, BRAIN,  
 PANCREAS AND LIVER.  
 -1- DISEASE: DEFECTS IN ARHGAP6 MAY BE A CAUSE OF MICROPHthalmia WITH  
 LINEAR SKIN DEFECTS (MLS), A DOMINANT MALE-LETHAL DISORDER  
 CHARACTERIZED BY EYE, SKIN AND CENTRAL NERVOUS SYSTEM (CNS)  
 MALFORMATIONS.  
 -1- SIMILARITY: CONTAINS 1 RHO-GAP DOMAIN.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 EMBL; AF117067; AAF43261.1;  
 EMBL; AF177663; AAD53166.1;  
 EMBL; AF177665; AAD55087.1;  
 EMBL; AF012272; AAC98539.2;  
 EMBL; AF022212; AAC98540.2;  
 HSSP; Q07960; 1RGP.  
 DR Genew; HGNC:676; ARHGAP6.  
 DR MIN; 300118;  
 DR MIN; 309801;  
 DR InterPro; IPR000198; RhoGAP.  
 DR Pfam; PF00620; RhoGAP; 1.  
 DR SMART; SM00324; RhoGAP; 1.  
 KW Alternative splicing; GTPase activation; SH3-binding.  
 FT SITE; 342 352  
 FT DOMAIN 411 564  
 FT VARSPLIC 1 203  
 FT VARSPLIC 196 196  
 FT VARSPLIC 637 658  
 FT VARSPLIC 659 974  
 FT VARSPLIC 726 765  
 FT VARSPLIC 766 974  
 FT CONFLICT 231 231  
 FT SEQUENCE 974 AA; 105973 MW; F7D63AE78720DB25 CRC64;  
 SQ  
 Query Match 2.5%; Score 100.5; DB 1; Length 974;  
 Best Local Similarity 18.6%; Pred. No. 9.9;  
 Matches 178; Conservative 99; Mismatches 294; Indels 385; Gaps 46;  
 QY 27 AGSGRGARGADTCGRMKA-----AARPLCVANEGVGPASRN----- 64  
 Db 51 AGAGSGARGA-TAG-RLYSPSLPAESGLPRLASSRSGPPPRATRLPPPGPLCSFSTPST 108  
 QY 65 -----SGLYNITFKYDNCITTYLNFVG-----KHVIADAQNIITISQYACHQVAVTILWS 113  
 Db 109 PQEKSPSG-----SFHED-----YEYPLGRGLKSMANDLPVSLAGPASSRSASSILCSSG 160  
 QY 114 PGALGIEFLAGFVILEELKSEGCQQLIKDPKQLNSSFRTGHSOPFLMKFETDY 173  
 Db 161 GGPNGI-----FASPRMLQORFQSPD-----SRGHPYVWVKSSEDF 199  
 QY 174 F-----VKVFPFSIKNESNY-----PFFETRACDILLQ-----PDNLACKPFWK 215  
 Db 200 TWSMSGRSVRLNSVPIQSLSELERARLQEVFPVYLOQDCDLSCQITIPKQOKRK---K 256  
 QY 216 PRNLINISQHSQDMQVSDFHAPHNCFREFYL-----HYLKH-----G 254  
 Db 257 SLRKKDISLGKRNKKEFIQAFQGLPUSQVIANRAYKLKQLQDRDEKQASDFVASLL 316

CC 255 PFKRTCKOE-----OTTETSCILQNVSP-----DYLIELVDD 289  
 CC 317 PGNKRONKELSSNSLSTSTPN---ESTSPATPEPAPARRRGAMSVSDYLDLDN 373  
 CC 290 TMTTRKVNH-----YALKPVHSPWAGPRAVAITVPLVWISAPATL- 330  
 CC 374 QSRLEALQSLPAEAKSKKARDKKLSLNPYR-----QVPLVDSCQHLE 422  
 CC 331 FVWCRKKQENIYSHLDE-----ESSESYYAALPRERLRPRKVEL- 374  
 CC 423 KIGLQTVGIPVSGSKKRRQLREEDRGIDVSLSEESVHDVAALKKEFLMDPDLT 482  
 CC 375 CTSS-----KQGHNVVQCFAVFLDFCCGEVALNWE-----DFSLCREG 417  
 CC 483 RELITAFINTLLLEPEQLGLTQLLYLPP-CNCDTLHRLQLFLSTVARHADNISKDG 541  
 CC 418 Q-----REWVIO-----KIHESOFIIVVCSKGMKFFYDK 446  
 CC 542 QSVTGNKMTSLNATIFGPNMLLHKQSSDKKESVQSSARAEESTAIIVVQKMI- 595  
 CC 447 KNYKKGGRSGGKGLFLVAVSATAEKL-----RQAKOSSAAL- 486  
 CC 596 ENYE-----ALFWPDLQNEVLISLELTDVDVYLLRRKASQSSPDLQSE 644  
 CC 487 VSFVSGRHSTDSNKASSGDISPYDNNSPILSERSLLAMOEADAAPGSEKLYRVPQFM 704  
 CC 508 L-----STKYRLMDNLPOLCSHL-----HSR-DHGLQPPGHTROGSRNRYPS 550  
 CC 705 LVGHLSKSSKSSPGRGLKOLSEPPDINGTWHSTILKSGRDPGH---TSSGDIPES 761  
 CC 551 KSGRLYVAINHMQFIDEEDPWFKEQFVPPHPPPLRTPREPLEKFDGLVLDVNCXPG 610  
 CC 762 S-----SLRAGPCSLSQG-NLSPNPRWQSGP-----AELDS- 792  
 CC 611 PESDFCLKVEANVLGATGAPDSOHESQHGGLDQGEARPALDQSAALQPLLHTVKGSPS 670  
 CC 793 DTQCARQTAQ-----APA-----TEGRAHPAVSRACSTPHVQVAGRAERT 834  
 CC 671 DMRED-----SGIDSSVPSSELSPLMEGLSTDQETTSSTESVSSSGGEEPP 722  
 CC 835 ARSEQYLTLSGADHLS-ESELDVAGLSRATPQCR-----PHGSGRDKRPP 881

RESULT 13  
 ID Z151.MOUSE  
 AC Q60821; 060699; STANDARD; PRT; 794 AA.  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE 16-Oct-2001 (Rel. 40, Last annotation update)  
 DE Zinc finger protein 151 (Polymavirus late initiator promoter binding protein) (LP-1) (zinc finger protein z13).  
 GN ZNF151 OR ZFP100.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID:10090;  
 RN [1]  
 RA Rapp L., Carmichael G.G.;  
 RL Submitted (APR-1995), to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RC STRAIN-CBA; TISSUE-Kidney;  
 RX MEDLINE-96003919; PubMed-7575457;  
 RA Schulz T.C., Hopwood B., Rathjen P.D., Wells J.R.E.;  
 RT "An unusual arrangement of 13 zinc fingers in the vertebrate gene z13."  
 RL Biochem. J. 311:219-224(1995).  
 CC -!- FUNCTION: MAY FUNCTION AS A HOUSEKEEPING DNA-BINDING PROTEIN THAT

CC REGULATES THE EXPRESSION OF SPECIFIC GENES.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -!- TISSUE SPECIFICITY: FOUND IN ALL THE EMBRYONIC AND ADULT TISSUES EXAMINED.  
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.  
 CC -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.  
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CC EMBL; U22396; AAA64848.1;  
 CC EMBL; U14556; AAA85493.1;  
 CC HSSP; P08046; 1A1H.  
 CC MGD; MGI:107410; Zfp100.  
 CC InterPro: IPR000210; BTB\_POZ.  
 CC InterPro: IPR000822; Znf\_C2H2.  
 CC Pfam; PF00056; Zf\_C2H2; 13.  
 CC Pfam; PF00651; BTB; 1.  
 CC PRINTS; PR00048; ZINC\_FINGER.  
 CC PRODOM; PD000003; Znf\_C2H2; 1.  
 CC SMART; SM00225; BTB; 1.  
 CC SMART; SM00355; Znf\_C2H2; 13.  
 CC PROSITE; PS00097; BTB; 1.  
 CC PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 13.  
 CC PROSITE; PS0157; ZINC\_FINGER\_C2H2\_2; 13.  
 CC Transcription regulation; DNA-binding; zinc-finger; Metal-binding;  
 CC Nuclear protein; Repeat.  
 CC DOMAIN 1 104  
 CC ZINC\_FINGERS.  
 CC FT DOMAIN 297 730  
 CC FT ZN\_FING 297 319  
 CC FT ZN\_FING 325 347  
 CC FT ZN\_FING 353 375  
 CC FT ZN\_FING 381 403  
 CC FT ZN\_FING 409 431  
 CC FT ZN\_FING 437 459  
 CC FT ZN\_FING 465 487  
 CC FT ZN\_FING 493 515  
 CC FT ZN\_FING 519 543  
 CC FT ZN\_FING 549 571  
 CC FT ZN\_FING 577 599  
 CC FT ZN\_FING 605 628  
 CC FT ZN\_FING 708 730  
 CC FT CONFLICT 507 507 G -> A (IN REF. 2).  
 CC FT CONFLICT 573 573 N -> K (IN REF. 2).  
 CC SEQUENCE 794 AA; 86664 MW; FFF80E56DEBF7ED CRC64;

Query Match 2.5%; Score 99.5; DB 1; Length 794;  
 Best Local Similarity 20.6%; Pred. No. 8.9;  
 Matches 71; Conservative 41; Mismatches 146; Indels 87; Gaps 15;  
 QY 399 CGCEVALDWEFSLCREGREWIQKIHESQFIIVVCSKGMK-YFVDKKNYKHGGGRG 457  
 DB 24 CDCTFVVD-CVDF-----KAHKA-VLAACSEYFKMLFVQKDVVHLDISNA 67  
 QY 458 SGKGEFLVAVSAIAEKLRQAKQSS-----AALSKFIATYFDYSCGDVPGILDIST 510  
 DB 68 AGIAGQ-----VLEFMTAKLSLSPENVDDVLAVASFQMQ-----DIVT 106  
 QY 511 KYRLMDNLPOLCSHL-HSRDHGLQBPQGH-----TROGSRNRYFKSGRSLY 557  
 DB 107 ACHTLKSLAEPSSTTGESADASAVEGGDKRAKDEKKAATMLSRGQARSSSTGPGRELK 166  
 QY 558 VAICNMHQFIDEEDPWFKEQFVPPHPPPLRTPREPLEKFDGLVLDVNCXPGSPDFCL 617  
 DB 167 EERGGQAESASSGAEQTEKADAPREPPP-----VELKPDPTSSMA- 206  
 QY 618 KVEAVALGATGAPDSQHSOHGGLDQGEARPALDQSAALQPLLHTVKGASPSDPRDSG 677

Db 207 ABAEALSSSEMEVEPASK--EDGDEECAGPATVKEGMH-LONGEPEENEESA 263  
 QY 678 IYDSSVPSSELSLP---LMEGLSDOTETSSLTSSVSSSGLGE 719  
 Db 264 GTDS---GOELGMEONLSRSTGYDRTEKSKAYGSIHKCEOCGE 305

RESULT 14  
 ZFY2\_MOUSE STANDARD; PRT; 783 AA.  
 AC P20662;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Zinc finger Y-chromosomal protein 2.  
 GN ZFY2 OR ZFY-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89168416; PubMed=2493989;  
 RA Mardon G., Page D.C.;  
 RT "The sex-determining region of the mouse Y chromosome encodes a  
 protein with a highly acidic domain and 13 zinc fingers.";  
 RL Cell 56:765-770(1989).  
 CC -!- FUNCTION: PROBABLE TRANSCRIPTIONAL ACTIVATOR.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
 FINGER PROTEINS. ZFY/ZFY SUBFAMILY.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M24401; AAA56845.1;  
 CC PIR; A31491; A31491.  
 CC DR HSSP; P08048; 52NF.  
 CC DR MGD; MGI:99213; zfy2.  
 CC DR InterPro; IPR000823; Znf\_C2H2.  
 CC DR Pfam; PF00096; zf-C2H2; 13.  
 CC DR PRINTS; PR00048; ZINCFINGER.  
 CC DR ProDom; PD000003; Znf\_C2H2; 1.  
 CC DR SMART; SM00355; Znf\_C2H2; 13.  
 CC DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_2; 10.  
 CC DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_1; 7.  
 CC DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 10.  
 CC KW Transcription regulation; Activator; zinc-finger; Metal-binding;  
 CC DNA-binding; Repeat; Nuclear protein.  
 CC FT DOMAIN 372 382 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 CC FT DOMAIN 403 777 ZINC FINGERS.  
 CC FT ZN\_FING 403 425 C2H2-TYPE.  
 CC FT ZN\_FING 434 456 C2H2-TYPE.  
 CC FT ZN\_FING 466 488 C2H2-TYPE.  
 CC FT ZN\_FING 497 520 C2H2-TYPE.  
 CC FT ZN\_FING 526 548 C2H2-TYPE.  
 CC FT ZN\_FING 554 577 C2H2-TYPE.  
 CC FT ZN\_FING 583 605 C2H2-TYPE.  
 CC FT ZN\_FING 611 634 C2H2-TYPE.  
 CC FT ZN\_FING 640 662 C2H2-TYPE.  
 CC FT ZN\_FING 668 691 C2H2-TYPE.  
 CC FT ZN\_FING 697 719 C2H2-TYPE.  
 CC FT ZN\_FING 725 748 C2H2-TYPE.  
 CC FT ZN\_FING 754 777 C2H2-TYPE.  
 CC SQ SEQUENCE 783 AA; 88856 MW; 1722D1C23F019DF8 CRC64;  
 Query Match 2.5%; Score 99; DB 1; Length 783;  
 Best Local Similarity 19.2%; Pred. No. 9.6;

Matches 117; Conservative 74; Mismatches 207; Indels 210; Gaps 34;  
 QY 71 TFKYDNCNTTLPVGRKHIADAGNITTSOYACHDOVAVTILMSPGALTEELKGRFVILE 130  
 Db 339 TAAYDNNSDEI-----EVQATASMLHDESG-----GLD-----RVPKQ 374  
 QY 131 ELKS-----EGRCQOQILKDPKQLNSSFRTGMSQP--FLNMKFTDYFVKVFPFPIK 184  
 Db 375 KSKKKRPESKOYSAIFVAPDQT-----LRVYCNFCGKKFKTRFLK-----RHIK 423  
 QY 185 NESNYHPPFFTRACDILLQPNLACKDFWKPRLNLSIQHSDNQVSPDPAHNEGFRFF 244  
 Db 424 N-----HPEYLANKY-----HCTEDYSTNKKIS----- 448  
 QY 245 YLHYKLKHEGPFRTCKOBTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALAPV 304  
 Db 449 -LHHMESH-----KLTKTEKTECCDC-RKNLSHA-----GTLCTHKTMTTE--- 490  
 QY 305 HSPWAGPIRAVAITVPLWVI---SAFATLFT---VMCRKKQOENIYSHLDESSSESTY 357  
 Db 491 -----KGVNKTCKCFCDYETAETILLNHLVVRKK-----FPHICGCGKGRFH 537  
 QY 358 TAALPRE-RLRPRPKVFLC---YSSKQDN---HMNVQCFAYFLQDFCGCEVALDLWE 409  
 Db 538 PSALKKHIRVHTGEKPEYCEYKSAOSSNLKTHSKSKKEIPK---CDICL---L 590  
 QY 410 DFSLCRGQREWI---OKIHESQFIIVCSKGMKYFVCKNKKYHKGGRGSGKGELFLV 466  
 Db 591 TFSDTKEAQOHAHVHOSRTHO-----CS-----HCNHESSNSDLKRHIISV 633  
 QY 467 AVSAIAKLRQAKQS---SSAALSKEPIAVFYDYS---CEGDVPG-----ILDSTK 511  
 Db 634 HTKAYPHKDCMCKSGFHRPSELKHHVATKSKMHQCHCDNSPDPFLLSHILLSAHT 693  
 QY 512 YRLMDNLPOLCSHLSEHDHGLQEPQHTROGSRNRYFSKSGSLYVAICNMHQFIDEEP 571  
 Db 694 -----NVFFCKCKCKK-----EFOOCELQTHMKTSSRKVYQ---CEYESTYKDA 737  
 QY 572 DMFEKQVFPFPPPLRYREPVLKEFDSGLVLDVNMCKPGPESDFCLKVEAAVILGATGP 631  
 Db 738 SGFKRRYVISHTRDYDHR-----CDFCKK-----GFRDPE 768  
 QY 632 -SHESOH 638  
 Db 769 KNQIMRH 776

RESULT 15  
 PSUL\_YEAST STANDARD; PRT; 970 AA.  
 AC PS3550;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE mRNA decapping protein 2 (PSUL protein).  
 GN DCP2 OR PSUL OR YNL118C OR N1917.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D273-10B;  
 RA Tzagoloff A.A.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97245296; PubMed=9090055;  
 RA de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,  
 RA Pallavicini A., Lanfranchi G., Valle G.;  
 RT "The DNA sequence of cosmid 14-13b from chromosome XIV of  
 Saccharomyces cerevisiae reveals an unusually high number of  
 overlapping open reading frames.";

RL Yeast 13:261-266(1997).  
RN [3]  
RP INTERACTION WITH DCP1.  
RX MEDLINE=99436017; PubMed=10508173;  
RA Duncley T., Parker R.;  
RT "The DCP2 protein is required for mRNA decapping in Saccharomyces  
RT cerevisiae and contains a functional Mutf motif.";  
RL EMBO J. 18:5411-5422(1999).  
CC -1- FUNCTION: REQUIRED FOR THE PRODUCTION OF ACTIVE DECAPPING ENZYME,  
CC PERHAPS IN A PROCESS REQUIRING THE HYDROLYSIS OF A PYROPHOSPHATE  
CC BOND. DECAPPING IS A THE MAJOR PATHWAY OF MRNA DEGRADATION IN  
CC YEAST. IT OCCURS THROUGH DEADENYLATION, DECAPPING AND SUBSEQUENT  
CC 5' TO 3' EXONUCLEOTIC DECAY OF THE TRANSCRIPT BODY.  
CC -1- SUBUNIT: INTERACTS WITH DCP1.  
CC -1- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. STRONG, TO  
CC S.POMBE SPAC19A8.12.  
CC -----  
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CC -----  
DR EMBL; L43065; AAA68866.1;  
DR EMBL; Z69382; CAA93389.1;  
DR EMBL; Z71394; CAA95998.1;  
DR SGD; S0005062; DCP2.  
DR InterPro: IPR000086; NUDIX\_hydrolase.  
DR Pfam: PF00293; NUDIX.1  
DR PRINTS; PR00502; NUDIXFAMILY.  
DR PROSITE; PS00893; NUDIX.1.  
KW Hydrolase.  
FT DOMAIN 134 155 NUDIX BOX.  
FT DOMAIN 436 439 POLY-SER.  
FT CONFLICT 425 425 P -> L (IN REF. 1).  
SQ SEQUENCE 970 AA; 108667 MW; D53CA2C5A546FA4A CRC64;  
  
Query Match 2.5%; Score 99; DB 1; Length 970;  
Best Local Similarity 17.9%; Pred. No. 13; indels 218; Gaps 26;  
Matches 106; Conservative 86; Mismatches 182;  
  
QY 274 LONVSPGDYIE--LV-----DNTTRKVMHYALAPVHSPW--AGPIRAVAITVP 320  
DB 9 LENVTSVDRILEDLVRFIINCNPEDLSVERELFHE-----EASWYTFDKLANPTLP 64  
QY 321 LVVISAPATLFTVCKRKKQENIYSHLDESESSSTYTAALP-----RERLR----- 367  
DB 65 SLKIKSPAQLIILKPLVWKNDI--RVDEALQFQSKYKKSIPVGGAAIFNENLSKILLVQ 122  
QY 368 -----PRPKVFLCYSSKDGQNMNVQCFAIFLQDFCGCEVALDLWEDFSLCREGQ 418  
DB 123 GTESDWSFPRGKI-----SKD-----ENDIDCIREVKE-----EIGFDLTD----- 160  
QY 419 REWVIQIHESQRIIVVCSKGMKYFVKKKYKHKGGGSGKGELELVA-VSAI----- 471  
DB 161 -----YIDNQFI-----ERNIQKNTR-----IFLISGVSEVENFKPQ 194  
QY 472 -----AEKLR--QAKQSSAALSFKFIATVFYDS-----CEGD 501  
DB 195 VRNEIDKIEWFDEFKIKTKMYKSNIKYTLINSMRPLSMWLRHQRIKKNEDQLKSYAEQ 254  
QY 502 VPGILDSTYRLMDNLPOLCSHLHR-----DHGLQEPGQHTR 540  
DB 255 LKLLIGI-TREEDIDPRELLAMLHATVQANNNNAVNSQVPSSELQHLKEQSGERNQ 313  
QY 541 QGSRNRTFSKSGSLYVAICN-----MHQFIDEEPWFE-----KOFVPPF- 581  
DB 314 QKQQSSFSQQQPSIFPSLSEPFANNKVIPTPMNAVFMNSNPQLFATMNGQFPADFP 373  
QY 582 -----HPPPLRYREPVLKFKDGLVNDVCKKPGFESDFC 616

DB 374 FMLPLTNNNSAMPITPVPPNFNAPPNMAFGVPNNHNLGFPAYSQPFSLPPAPL----- 429  
QY 617 LKVENAVLGCATGPADSOHESOHGG--LDODGEARPALDGSAAALOPLLHTVTKAGSPSDMPR 674  
DB 430 -----PROSGYSSSPGQLLDILNSKKPDSNVQSSKKPKLKILQRGTDLSIK 477  
QY 675 DSGIYDSSVPSSSELSPLMEGLSTDQ-----TETSLTESVSSSSGLGEEE 720  
DB 478 QNNNDETAHNSQALIDLKPKTSSQKIHASKPDTSELPN--DSVSGIQDAE 527

Search completed: May 6, 2003, 13:43:05  
Job time : 22 secs



QY 370 PKVFLCYSSKDGQNHVYVQCFAYFLQDFCCEVALDWDWDFSLCREGQRENVIOKIHES 429  
 DB 181 PKVFLCYSSKDGQNHVYVQCFAYFLQDFCCEVALDWDWDFSLCREGQRENVIOKIHES 240  
 QY 430 QFIIIVCSKGMKYFVDKKNKKGGRSGGSGELFLVAVSAIAEKLRQAKQSSAALSFP 489  
 DB 241 QFIIIVCSKGMKYFVDKKNKKGGRSGGSGELFLVAVSAIAEKLRQAKQSSAALSFP 300  
 QY 490 IAVFYDSCGDVPGIILDLSTKYRLMDNLPOLCSHLSDHGLQEPQHTROGSRNRYR 549  
 DB 301 IAVFYDSCGDVPGIILDLSTKYRLMDNLPOLCSHLSDHGLQEPQHTROGSRNRYR 360  
 QY 550 SKSGRSLYVAICNNHOFIDEEPDPKOFVFPFPPPLRYREPVLKFDGSLVNDVMCKP 609  
 DB 361 SKSGRSLYVAICNNHOFIDEEPDPKOFVFPFPPPLRYREPVLKFDGSLVNDVMCKP 420  
 QY 610 GPESDFCLKVEAAVATGATPADQSQHSQHGGLDQDGEARPDGSAALQPLHTYKAGSP 669  
 DB 421 GPESDFCLKVEAAVATGATPADQSQHSQHGGLDQDGEARPDGSAALQPLHTYKAGSP 480  
 QY 670 SDMPDSDGIYDSSVPSSELSPLMEGLSTDOTETSSLTESVSSSGIGREPPALPSKLL 729  
 DB 481 SDMPDSDGIYDSSVPSSELSPLMEGLSTDOTETSSLTESVSSSGIGREPPALPSKLL 540  
 QY 730 SSGSKADLCGRSYTDELHVAAPL 753  
 DB 541 SSGSKADLCGRSYTDELHVAAPL 564

## RESULT 2

Q8R5J8 PRELIMINARY; PRT; 582 AA.  
 AC Q8R5J8:  
 DT 01-JUN-2002 (TRENBLrel. 21, Created)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Similar expression to FGF protein (Fragment).  
 GN SEF.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21824237; PubMed=11802165;  
 RA Furthauer M., Lin W., Ang S.L., Thiese B., Thiese C.;  
 RT "Seif is a feedback-induced antagonist of Ras/MAPK-mediated FGF  
 signaling".  
 RL Nat. Cell Biol. 4:170-174(2002).  
 DR EMBL; AF424804; AAL79530.1;  
 FT NON\_TER 1  
 SQ SEQUENCE 582 AA; 65263 MW; 56663B2981C4268E CRC64;

Query Match 65.2%; Score 2616.5; DB 11; Length 582;  
 Best Local Similarity 84.6%; Pred. No. 5.6e-231;  
 Matches 496; Conservative 34; Mismatches 49; Indels 7; Gaps 4;  
 QY 171 TDYEVKVVPPSPKSNESNHPFFTRACDILLQPDNLACKPWRPNLNISQHSQDMOV 230  
 DB 1 TDYEVKVVPPSPKSNESNHPFFTRACDILLQPDNLACKPWRPNLNISQHSQDMOV 60  
 QY 231 SFDHAPNFGFRFYLYHKLHKGFPKRTCKQBTETTSCLLNQSPGDYIELVDDT 290  
 DB 61 SFDHAPNFGFRFYLYHKLHKGFPKRTCKQBTETTSCLLNQSPGDYIELVDDT 120  
 QY 291 NTRKVAHYALKRPHVSNAGPIRAVAITPLVWISAFATLFTVCKRKKQENIYSHLDEE 350  
 DB 121 NTRKVAHYALKRPHVSNAGPIRAVAITPLVWISAFATLFTVCKRKKQENIYSHLDEE 180  
 QY 351 SSESSTYALPRERLRPRPKVFLCYSSKDGQNHVYVQCFAYFLQDFCCEVALDWDW 410  
 DB 181 SPESSTYALPRERLRPRPKVFLCYSSKDGQNHVYVQCFAYFLQDFCCEVALDWDW 240

QY 411 FSLCRGQRENVIOKIHESQFIIIVCSKGMKYFVDKKNKKGGRSGGSGELFLVAVSA 470  
 DB 241 FSLCRGQRENVIOKIHESQFIIIVCSKGMKYFVDKKNKKGGRSGGSGELFLVAVSA 300  
 QY 471 IAEKLRQAKQSSAALSFPFIIVFYDSCGDVPGIILDLSTKYRLMDNLPOLCSHLSDH 530  
 DB 301 IAEKLRQAKQSSAALSFPFIIVFYDSCGDVPGIILDLSTKYRLMDNLPOLCSHLSDH 357  
 QY 531 GLQEP--GQHTROGSRNRYRFRSKGRSLYVAICNNHOFIDEEPDPKOFVFPFPPPLRYR 589  
 DB 358 GEQEVLGQHPGHSRRNRYRFRSKGRSLYVAICNNHOFIDEEPDPKOFVFPFPPVRYQ 417  
 QY 590 EPLVLEKFDGSLVNDVMCKPESDFCLKVEAAVATGATPADQSQHSQHGGLDQDGEA 647  
 DB 418 EPLVLEKFDGSLVNDVMCKPESDFCLKVEAAVATGATPADQSQHSQHGGLDQDGEA 477  
 QY 648 RPAIDGSAALQPLHTYKAGSPDMPDSDGIYDSSVPSSELSPLMEGLSTDOTETSSLT 707  
 DB 478 QPSCDSAPALQPLHTYKAGSPDMPDSDGIYDSSVPSSELSPLMEGLSTDOTETSSLT 537  
 QY 708 EYSSSSGIGREPPALPSKLLSGSKADLCGRSYTDELHVAAPL 753  
 DB 538 EYSSSSGIGREPPALPSKLLSGSKADLCGRSYTDELHVAAPL 582

## RESULT 3

Q8QHJ9 PRELIMINARY; PRT; 745 AA.  
 AC Q8QHJ9:  
 DT 01-JUN-2002 (TRENBLrel. 21, Created)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Seif.  
 GN SEF.  
 OS Brachydanio rerio (Zebrafish) (Zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21824236; PubMed=11802164;  
 RA Tsang M., Friesel R., Kudoh T., Dawid I.;  
 RT Identification of Seif, a novel modulator of FGF signalling".  
 RL Nat. Cell Biol. 4:165-169(2002).  
 DR EMBL; AF364103; AAL76112.1;  
 SQ SEQUENCE 745 AA; 83431 MW; 56FE1F0B9D98DB4 CRC64;

Query Match 48.9%; Score 1961; DB 13; Length 745;  
 Best Local Similarity 51.4%; Pred. No. 1.1e-170;  
 Matches 390; Conservative 114; Mismatches 197; Indels 58; Gaps 10;  
 QY 1 MAPMLQCSVFTTVNACLSQLAFAAGSGRGARGADTCGWRKAKAAARPLCVANEGVGP 60  
 DB 7 LAHFFNASCFLCYTASVNG-----GKRGNSDKCSYK-----OQTQT 43  
 QY 61 ASRNSGL--YNTFFYDNCCTYLPVGVKHIADAQNTISQVACHDQVAVTILMSPCALG 118  
 DB 44 SSWDEGARLGVTFYDNCNVNPNPLGKHAHEVNNTFSHLSQDSQAQVAVVHMASPLG 103  
 QY 119 IEPLGFRVILELSKGRQCCQQLILKDPQLNNSFKRTGMSQFPLMKFETDYFKVV 178  
 DB 104 IEHVGFRVYLEDKKNPERKQCOHLILKDPQLNNSFKRTGMSQFPLMKFETDYFKVV 163  
 QY 179 PPSIKNESNYHPFFTRACDILLQPDNLACKPWRPNLNISQHSQDMOVSDPHAPN 238  
 DB 164 PPTPLNDSEFPSPPLRTNSCEVLGPDNLVCKPWRPNLNISQHSQDMOVSDPHAPN 223  
 QY 239 FGFRFYLYHKLHKGFPKRTCKQBTETTSCLLNQSPGDYIELVDDTNTTKVHH 298  
 DB 224 FGFRFYLYHKLHKGFPKRTCKQBTETTSCLLNQSPGDYIELVDDTNTTKVHH 283

QY 299 YALPVPVSHWAGPIRAVAITVPLVVISAFATLFTVCRKQOENIYSHLDESESSST 358  
 DB 284 YHVSQVSHWAGPIRAMAITVPLVVISAFATLFTVCRKQOENIYSHLDESESSST 343  
 QY 359 AALPRELRPRKPVLCYSSKDGONHNVVQCFAYFLQDFCCEVALDLMEDFSLCREG 418  
 DB 344 TALSADRPWRPKPICTYSSRDGAKHLAVIQSFAPFLQDFCCEVSLDLWEHLICKEG 403  
 QY 419 REMVIOKIHESQFIIVVCSKGMKVFYDKNYKHGGGR-----GSGKGEFLVA 467  
 DB 404 MSWLSRRIDEAHLFTVCSKGLKHFVEKRKCKATSKENREPSASDSSSSRDLEIVA 463  
 QY 468 VSAIAEKLRQAKQSSAALSFIAYDYSCEDVPGILDSTKYRLMDNLPOLCSHLHS 527  
 DB 464 SAIISSEKLEVKHQS--DLRFNSVTFDYSHETDPTSLAPKFLMDQUPQLFARLHS 522  
 QY 528 RDHGLQEPQOHTROGSRNRYFRSKSGSLVVAICNNHOFIDPEDFKQVPPHPLR 587  
 DB 523 RQLSLTDREPOPNNVSKRNYFCSSKSGSLVVAIYNHGHVTOEPWLEKELM---PPPLP 579  
 QY 588 YREPVLKEDFSGVLNDVCMKPGPESDFCLKVEAAVL-----GATGPADSQSHSOGG 640  
 DB 580 NKRTIPKVDYSGVLNVEYKLGHSESE--CPPVRSNVLLPOTPVGVSVLSLREDLEGS 638  
 QY 641 LDQGEARPALDGSAAQLPLHTVKGASPDMPROSGIYDSSVSPSELSPLMGLSTQ 700  
 DB 639 SSQD-----AGSCRPLVLTGDSASPPENPRDGIYDSSVSPSELSPLMDGLSPDH 689  
 QY 701 TETSSLTESVSSSGLGEEPPALPKLLSSGS--CKADL 738  
 DB 690 ADNSSLADSVSSSGLGDEEPPAVSSLHCTAHTICKADL 728  
 RESULT 4  
 ID Q9NA64 PRELIMINARY; PRT; 745 AA.  
 AC Q9NA64;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE FGF signaling antagonist Sef.  
 GN Sef.  
 OS Brachydanio rerio (Zebrafish) (Zebra dario).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21824237; PubMed=11802165;  
 RA Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.;  
 RT "Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF  
 signaling."  
 RL Nat. Cell Biol. 4:170-174(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Furthauer M., Lin W., Siew-Lan A., Thisse B., Thisse C.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR ENBL: AF401232; AAL78817.1;  
 SQ SEQUENCE 745 AA; 83437 MW; 75B9EDCC08A4652 CRC64;

Query Match 48.6%; Score 1952; DB 13; Length 745;  
 Best Local Similarity 51.1%; Pred. No. 7.6e-170;  
 Matches 388; Conservative 116; Mismatches 197; Indels: 58; Gaps 10;  
 QY 1 MAPWLQCSVFTVACNLGSLAVAGSGRGARGADTCGRWKAARPRLCVANEVGP 60  
 DB 7 LAHFFVACSLFLCYTASVNG-----GKRGNSDKCSYK-----QSTQT 43  
 QY 61 ASRNSGL--YNTFFKDYNDCTYLPVKGKHYADAQNTISQYACHQDVAVVTLNPGALG 118  
 DB 44 SSNDGKARGLVTFYDNCVSNWSPGLGKHAHEVNNISFSLSCDSQAQVAVVHNASPLG 103

QY 119 IEPLAGFVILKEKSEGOOQOOLILKDPKQNSGFKRTGMSOPFLNMFETDYFKVYV 178  
 DB 104 IEHVGFVILKEKSEGOOQOOLILKDPKQNSGFKRTGMSOPFLNMFETDYFKVYV 163  
 QY 179 PPSKINSNTHPFFTRACDILLQPDNLACKPFWKPRNLNISOHSDQVQSFDAHPN 238  
 DB 164 PPNFLNDSFPFPPFLNDSCEVLLGPDNLCKPFWKPRNLNISOHSDQVQSFDAHPN 223  
 QY 239 FGRFFYLYKHLKHEGPFKRTKQEQYTTETTSCLQNVSPQDITIELVDQNTTTRKVMH 298  
 DB 224 FGRFFYLYKHLKHEGPFKRTKQEQYTTETTSCLQNVSPQDITIELVDQNTTTRKVMH 283  
 QY 299 YALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCRKQOENIYSHLDESESSST 358  
 DB 284 YHVSQVSHWAGPIRAMAITVPLVVISAFATLFTVCRKQOENIYSHLDESESSST 343  
 QY 359 AALPRELRPRKPVLCYSSKDGONHNVVQCFAYFLQDFCCEVALDLMEDFSLCREG 418  
 DB 344 TALSADRPWRPKPICTYSSRDGAKHLAVIQSFAPFLQDFCCEVSLDLWEHLICKEG 403  
 QY 419 REMVIOKIHESQFIIVVCSKGMKVFYDKNYKHGGGR-----GSGKGEFLVA 467  
 DB 404 MSWLSRRIDEAHLFTVCSKGLKHFVEKRKCKATSKENREPSASDSSSSRDLEIVA 463  
 QY 468 VSAIAEKLRQAKQSSAALSFIAYDYSCEDVPGILDSTKYRLMDNLPOLCSHLHS 527  
 DB 464 SAIISSEKLEVKHQS--DLRFNSVTFDYSHETDPTSLAPKFLMDQUPQLFARLHS 522  
 QY 528 RDHGLQEPQOHTROGSRNRYFRSKSGSLVVAICNNHOFIDPEDFKQVPPHPLR 587  
 DB 523 RQLSLTDREPOPNNVSKRNYFCSSKSGSLVVAIYNHGHVTOEPWLEKELM---PPPLP 579  
 QY 588 YREPVLKEDFSGVLNDVCMKPGPESDFCLKVEAAVL-----GATGPADSQSHSOGG 640  
 DB 580 NKRTIPKVDYSGVLNVEYKLGHSESE--CPPVRSNVLLPOTPVGVSVLSLREDLEGS 638  
 QY 641 LDQGEARPALDGSAAQLPLHTVKGASPDMPROSGIYDSSVSPSELSPLMGLSTQ 700  
 DB 639 SSQD-----AGSCRPLVLTGDSASPPENPRDGIYDSSVSPSELSPLMDGLSPDH 689  
 QY 701 TETSSLTESVSSSGLGEEPPALPKLLSSGS--CKADL 738  
 DB 690 ADNSSLADSVSSSGLGDEEPPAVSSLHCTAHTICKADL 728

RESULT 5  
 ID Q9NA64 PRELIMINARY; PRT; 846 AA.  
 AC Q9NA64;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE Y64G10A.6 protein.  
 GN Y64G10A.6  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR ENBL: AL110498; CAB54470.1;  
 SQ SEQUENCE 846 AA; 94852 MW; 613AEF55EBB89EA4 CRC64;  
 Query Match 4.2%; Score 170.5; DB 5; Length 846;



Best Local Similarity 21.4%; Pred. No. 2.5e-06;  
Matches 141; Conservative. 82; Mismatches 225; Indels 211; Gaps 37;

QY 99 QYACHDOVAVILMSGALGIFLKGFRVILEELKSGROCOOLILKDPKQLNSSFRTG 158  
DB 294 QY-CFEEYEVRLDSS---GIVMLQSAIITDELRT---IINGRPVQGEF----- 338  
QY 159 HESQFPLNMFETDYFKVVPFSSKSNESNTHPFFTRACDILLQDNLAC-KFVKPR 217  
DB 339 ---NFTDIELDILPSVIPESAH---GRC-LCVTENCSCLAADWKP 382  
QY 218 MLNISQSGDKVQSFORAHNFGFRFFVILYKLKHEGFFKRTCKOEOTTTTSCLLQNV 277  
DB 383 KLT-----RIEKPATSN-----QTEESDGAEDKEDTTT----- 415  
QY 278 SPGDYIIELVDDNTTRKVMH-YALKPVHSPWAPIRAVATVPLVVISAFATL--FTVM 334  
DB 416 -----WHTYA-----ITGGAIILAILFSLVCAGLKCYKF 445  
QY 335 CRKQXQENIYSHLDESSESTYTAALPRERLPRKPVFLCYSSKQGNHNVQCFAYF 394  
DB 446 NKKKASNI--HLINENPAPS-HSGSIPL-ILKOSISVLIVY-SHDSAQHEAAVLAFEL 500  
QY 395 LQDCGCEVALDWEQFSLCRGOREWVIOKIHESQFLIVVCSKGMKYFDKNYKHGG 454  
DB 501 LQDVFNLVHLDWDEDI--EENRAEYINSSIVRANKVIINSIG-AYF--RTVFRHOR- 555  
QY 455 GRGSGKEFLVAVSAIAEKLRQAKSSAALSKEIAVYDYSCEGDV--PGILDSTKY 512  
DB 556 -----EPAERITTRND-----VIFDMOCELALQHPCVISCHFSY 591  
QY 513 -----RLMD-NLPOLCSHLSDHGLQEPGQHTROGSRNVFVSKSRLYVAI 560  
DB 592 TPKVVPFPIINLLOVSIIP--NSLMTWTALTQPARPQLAGFNQVFAF-----LQAI 644  
QY 561 CMNHQFIDEEPWFKEK-----QFVPHPPPLRYR----- 589  
DB 645 SRKLNIESQFQFENTHVRVATRRVSELEAHNVPL-PFSLVKVVEDEAFQOMETLPI 703  
QY 590 EFLVEKF-----DSGLVNDVMCKPSPESDFCLKVEAAVLGATGAPDSOHES 636  
DB 704 DELAKEFAAKRDLEVEVLDSEVDKLELVKCAPG-----IHYEPEVLEPAEPEE 758  
QY 637 QHGGLDQDGEARPALDSAA---LQPLT-HTVKAGSPDMPSDSCIYDSS-VPSSELS 689  
DB 759 AEDD-EEDDDVDSVQETARIEELQRLVH-----KONHDSGLNLSAYVSGSDFS 809

RESULT 6.  
ID Q99755 PRELIMINARY; PRT; 562 AA.  
AC Q99755;  
DT 01-MAY-1997 (T-EMBLrel. 03, Created)  
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
DE 68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha (EC 2.7.1.68).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97115834; PubMed=8955136;  
RA Lofjens J.C.; Anderson R.A.;  
RT "Type I phosphatidylinositol-4-phosphate 5-kinases are distinct  
members of this novel lipid kinase family."  
RL J. Biol. Chem. 271:32937-32943(1996).  
DR EMBL; U78576; AAC50911.1;  
DR InterPro; IPR002498; PIP5K.  
DR Pfam; PF01504; PIP5K; 1.  
DR SMART; SM00330; PIPK; 1.  
KW Kinase; transferase.

SQ SEQUENCE 562 AA; 62633 MW; ABF7988EB73506A0 CRC64;  
Query Match 2.9%; Score 117.5; DB: 4; Length: 562;  
Best Local Similarity 18.1%; Pred. No. 0.098;  
Matches 133; Conservative 105; Mismatches 239; Indels 257; Gaps 35;

QY 53 VANEGVGPASRSGNLYNIFKYNCTT-----YLPVGRVIAADONITISQVACHDOV 106  
DB 1 MASASGSPSS-SVGFSSDPAPVPSCTLSSAAGIKRPMASEVLEARQDSYLSLV----- 53  
QY 107 AVTILSPGALGIEFLK-GFRVILEELKSGROCOOLILKDPKQLNSSFRTGMSOPFL 165  
DB 54 -----PVASGMPKIKKHSRSDSGSETTYKTTSSALKGAIQLGIGTHTVGSLSRPER 106  
QY 166 NMFEFDYFKVVPFSS-----IKNESYHPPFFTRACDILLQDNLACKPFKPRNLNI 221  
DB 107 DVLMDQFVYVESIFFPSGCSNLTPAHYNDPRKTA----- 143  
QY 222 SQHSGDMQVSDHAPNFGFR---FFY-----LHYKLKHEGFFRKT 260  
DB 144 -----PVAFYFRELFGIRPDYLYSLASELIELCSCGASGLFT-VSSDDEFIKT 195  
QY 261 CKQBOTTTTSCLLQNVSPGDYIIELVDDNTTRKVMHVALKPVHSPWAPIRAVATVP 320  
DB 196 VQKEAB-----FLQKLLPGYIM-----NLQON-----P 219  
QY 321 LVVISAPATLFTVMCKKQ-----QENIYSHLDESSESTYTAALPRERLPRP 370  
DB 220 RTLLPKFYGLYCVQAGGNIRIVVNNLLPRSVKMKHIKYLKGSYTKRRASOKEREPLP 279  
QY 371 KVFELCYSSKQGNHNVQCFAYFLODF-CGCEVALDWEQFSLCRGOREWVIO---KI 426  
DB 280 -----TFKD-----LDFLQDIPDGLFADMYN--ALCKTLQRCVLQSFKI 320  
QY 427 HESQFIIV-----CSKGMKYFDKNYKHGGSGKGEFLVAVSAIAEKL 476  
DB 321 MDYSLILMSHINIDHAQREPLSSETQYSDTR-----RPAOKALYSTAMESIQGEAR 372  
QY 477 Q-----AKOSSAALSKEIAVYFYDYSCEGDVPGILDSTKYRLMDNLPOLC 522  
DB 373 RGTMTETDDHMGGIPARNKSGERLLLYI-----GIIDILQSYRFRVKKLEHSW 419  
QY 523 SHL-HSRDH-GLQEPGQHTROGSRNVFVSKSRLYVAICNMHOFIDEEPWFKEQFVP 580  
DB 420 KALVHGDVTVHVRGQFYAERFOR-----FQCN-----TVFEK--IP 454  
QY 581 FHPPPLRYREPVLKFDGSLVNDVMCKPSPESDFCLKVEAAVLGATGAPDSOHESQHG 640  
DB 455 LKPSPK-----KFRSG---SSFSRRAGSSGNSCITYQPSVSG-----EHKAQ--- 494  
QY 641 LQDGEARPALDSAAALPPLHTVKAGSPDMPSDSCIYD-----SSVPSSELSPLMEGL 696  
DB 495 -----VITKAEVPEGVH---LGRPDVLPQTPLEIEISGSPIDPSPFS-PLV-GE 539  
QY 697 STDQTESSLSIESV 710  
DB 540 TLQMLTSTTLEKL.553

RESULT 7.  
ID 013399 PRELIMINARY; PRT; 757 AA.  
AC 013399;  
DT 01-JAN-1998 (T-EMBLrel. 05, Created)  
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
DE Telomere-associated recQ-like helicase (Fragment).  
GN UTASRECO.  
OS Ustilago maydis (Smut fungus).  
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
OX NCBI\_TaxID=5270;  
RN [1]

RP: SEQUENCE FROM N.A.  
 RC STRAIN: FB2  
 RA Sanchez-Alonso P., Guzman P.,  
 RT Organization of chromosome ends in *Ostia* maydis: recQ-like  
 RL helicase motifs at telomeric regions.  
 DR EMBL: AF030885; A035264.1;  
 DR InterPro: IPR001410; DEAD.  
 DR Pfam: PF00370; DEAD.1;  
 DR SMART: SM00490; HELIC\_C.1;  
 DR ATP-binding; Helicase.  
 FT NON TER  
 SQ SEQUENCE 757 AA; 84382 MW; 1AE1E144353877 CRC64;  
 Query Match 2.9%; Score 117; DB 3; Length 757;  
 Best Local Similarity 20.4%; Pred. No. 0.17;  
 Matches 111; Conservative 56; Mismatches 187; Indels 190; Gaps 27;  
 QY 268 ETTICLLQVSPGDIIELVDDNTTRKVMHYALPVPSPWAGPIRAV-----AITVPL- 321  
 DB 77 ETTILIPVALRANLAKLVNN-----IRYVWQP-GSKKAPVILVSTERAITLAFKE 131  
 QY 322 -----VVISAFATLFTVCKKQKQENIYSHLDESSSTYTAALP----- 362  
 DB 132 YANRLQOQRLDRIVIDECHLTUTARSRRSMOLAHVRVETOTVLMLATIPFEDA 191  
 QY 363 --RERLRPRKVF-----LCYSSKQGNHNVVOCF-AYFLQDFCGCEVALDWEDF 411  
 DB 192 FISHNKLKPLIVRESTNRNLCYSVTAERHSMGTCYDAVRVD--ECRARTDIW--- 246  
 QY 412 SLRCGREGWYQKHESQFTLVVCSKMKYFYDK-----KNYKHGGGRS----- 458  
 DB 247 ----NGORD-----RIIVCTYS--KELVARLAEMLCAYSSGSEADKAAITQ 290  
 QY 459 ----QKGEFLVAVSAIAEKLROAKOSSAALSKFIAYFYDSCGVPGL--DLSTKY 512  
 DB 291 DMICGKSPVIVATSA-----LVGVFYHVRVFIHLGPDLLTDF 331  
 QY 513 -----RLMDNLPLCLSHLSRDLGLOEPGQHTROGSRNRYFS 550  
 DB 332 SQESGRAGCGMPAESILLACPLDORAP--ASGKASSAEKQVAP---ADKEMQLYRS 387  
 QY 551 KGRSLYVAICNMHOFIDEEDWPFKQFVFPHPPLRYREPVLKFDGSLVNDVMCKPG 610  
 DB 388 RK-----YCLRGVLSQLDORSW-----RWCMEGDQLCSVC 419  
 QY 611 PESDFCLKVEAAVLGATGPADSON---ESQHGGLDQGEARPALDGSAAALQPLHTVKAG 667  
 DB 420 PGCHF-----QAGPGQDFHTAPAGADPSTQSRHPSMHGSS--HPSNH----- 463  
 QY 668 SPSPMDRSGIYDSVPSSE--LSLPLMEGLSTDTTSTSLTESVSSS---SGLGESEPPA 723  
 DB 464 -----GSSHPSSSHSPHSIHGSHSGSS--HPSIHGSGHGQORRQKQPD 510  
 QY 724 LPSK 727  
 DB 511 PPSE 514  
 RESULT 8  
 O81789 PRELIMINARY; PRT: 917 AA.  
 ID O81789  
 AC O81789;  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Hypothetical 101.6 kDa protein.  
 GN F8D20.70 OR A4G35360.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eutroids II; Brassicales; Brassicaceae; Arabidopsals.  
 OX NCBI\_TaxID=3702;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Koetter P., Hempel S., Entian K.-D., Hohelsel J., Jesse T.,  
 RL Heljnen L., Vos P., Mewes H.W., Mayer K.F.X., Schueller C., Bevan M.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS).  
 DR EMBL: AL031135; CAA20026.1;  
 DR EMBL: AL161587; CAB80272.1;  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00400; WD40.2;  
 KW Hypothetical protein; Repeat; WD repeat.  
 SQ SEQUENCE 917 AA; 101552 MW; 1809BDC42302C820 CRC64;  
 Query Match 2.9%; Score 117; DB 10; Length 917;  
 Best Local Similarity 18.3%; Pred. No. 0.23;  
 Matches 167; Conservative 130; Mismatches 296; Indels 320; Gaps 42;  
 QY 19 NGSOLAAVAGSGRAGADTCGRM--KAAARPR-----LCVANEGV----- 58  
 DB 92 NGSRSV-----GYSNG-DILLWSIPSGECPSSAMICKNLGYKSEKIPTASLKWY 145  
 QY 59 --GPASR-----NSGLYNTFYDNCYTLNPKHV---IADAQNI--TISYACHDQ 105  
 DB 146 AEGKASRYVYSSNSLQVLLNEQTETRMILGLHVSEPCADMEMIADVNESSKHKQ 205  
 QY 106 VAVTILASPAIGT--EFLKGRFVILEELKSGROCOQILKDFKQNLNSFRKTGYESP 163  
 DB 206 DFLFVLGKSRVAYDDYMIKYLQSQSKSPSLPKETVVKLPSPSSITVKGFLTP 265  
 QY 164 --ELNMFETDY-----FVKVVPSPISKNESN---YHPFF-----FTRACDILLQPD 206  
 DB 266 SHLLWLSDE--DYAQLAKADAVPLPFTVTPKSSRSNAHPGFTKVKNYITGHCQGTISW 324  
 QY 207 NLACK-----PFWKPR-NLNIQHG-----SDMQVSPDHAPHNFRFRFYLYH 248  
 DB 325 DMTCSPFLVFLFKEQIDQDVSSRGNALTAHLHYDSNRLVSCDHNGMYVLYRFPKPEY 384  
 QY 249 KLKH-----EGPFKR-----KTCQEOETTETCLLQNVSP-----GDYIELV 287  
 DB 385 LTENSFPFGSLKGNHNVQSVKYLKTSITCIQSKNSKHLAIGSDGHDLSVEVI 444  
 QY 288 DDTNTRKVMHYALKPVHSPWAGPIRAVAVTVPLVIVAFATLFT----- 332  
 DB 445 D-----ALTPVY-----LOVSLVDIEANVLYTHIASDICPGIISIQ 482  
 QY 333 -----VNCRKQKENIYSHLDESSSTVTAALPRERLPRKPVLCVSSKD 380  
 DB 483 PESCIVOGFEKNVLVAMRDSVFA--LSDTGNMIGTNMFKP-----RPFKVLNQILD 536  
 QY 381 GONHNVVQCFAYFLQDFCGCEVALDWEDSLCRGREGWYQKHESQFTLVVCSK 437  
 DB 537 GK-----QDTSG-----NGFTSRES-----TVEEISIRQPSVLVCSKA 571  
 QY 438 -----KGMKIFYDKNKYKHKG-----GGRSKGRGELFLVAVSAIAE-----K 474  
 DB 572 IYIYSLAHVQVYKVKVHLKKESSPICSAFTFGTSGV---LTLVFTDGTGIVTSRSLPE 628  
 QY 475 LRQAKQS-----SSAALSKFIAYFYDSCG-----VPGILDSTKYRLMD 516  
 DB 629 LSQLKQTSIRGFTYSSPKNSPLPITISASMDGLVMVNGDDELIVSSVLPQKFTFLVE 688  
 QY 517 NLPOLCSHLHSRDLGLOEPGQHTROGSR-----NYFRSKSGSLVAVICNMHOFIDEE 570



RP SEQUENCE FROM N.A.  
 RC STRAIN-C-125/JCM 9153;  
 RX MEDLINE=20512582; PubMed=11058132;  
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kubara S.,  
 RA Horikoshi K.  
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
 RT halodurans and genomic sequence comparison with Bacillus subtilis."  
 RL Nucleic Acids Res. 28:4317-4331(2000).  
 CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY  
 CC (ABC TRANSPORTERS).  
 DR EMBL; AP001510; BAB04773.1;  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR003439; ABC\_transporter.  
 DR InterPro; IPR002559; Transposase\_11.  
 DR Pfam; PF00005; ABC\_tran; 1; 1;  
 DR Pfam; PF01609; Transposase\_11; 1.  
 DR ProDom; PD000006; ABC\_transportr; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER; 1.  
 DR ATP-binding; Transport; Complete proteome.  
 KW SEQUENCE 901 AA; 104585 MW; 5519406650B2CBB CRC64;

Query Match 2.94; Score 116.5; DB 16; Length 901;  
 Best Local Similarity 19.68; Pred. No. 0.25;  
 Matches 112; Conservative 76; Mismatches 169; Indels 215; Gaps 27;

QY 61 ASRNSGLNITFKYDCTTYLNPVKHVIADQNTISQY-ACHQDVAVTILWSPGALGI 119  
 DB 333 ALKESGL-----PLPKTLIADAGYGSNVADELPELTPIS----- 371  
 QY 120 EFLGPRVILELKSBR-----CCQOL--ILKDKQLNSPKKTCMESQPLNKKF 169  
 DB 372 ---HTFR--QEKRRSPAKRHPYNWRDETDVWCNQRKVFRTKTKTDY----GY 423  
 QY 170 ETDYFV-----KVVPF-PSI-----KNESNYHFFFRTRACDLLOPDLNACKPFWKPR 217  
 DB 424 ARDFKVECESECGGPFPECTKARGNRQVHPVY-----EELKAKQHOKLK 471  
 QY 218 NLNLSQHG-----SDMOVSDHAPNFGFFRYLVHKLKHEGPKRCKEQETTET 269  
 DB 472 ---SEGRTRYKRTDVSFVGVKQNLGFRRLHRC----- 507  
 QY 270 TSCLLQNSGDIYIELVDNTTRKVNHALKVPVSPWAGPIRAVAITVPLWIS-AFA 328  
 DB 508 -----ESVHIELGLVALAHLR 524  
 QY 329 TLFVVMCRKQOENIYSHLDESSSESYTAALPRRLPRKPVLCYSSKDGONHNVV 388  
 DB 525 KRATVDRSRKEPKNTNQHNEN-----RIKRF-----SRFYVL 558  
 QY 389 QCF---AYFLDFCCGEVALDLWEDFSLCREGQEW---TQKHESQFIIVVCSKMG 441  
 DB 559 RCWDSFFKIKGQKQYASFAFD--KLREGGENMIEVILDSKTYRNRQV---KGIN 612  
 QY 442 YFDKKNYHKGGGSGKGLFLVAVSAI-----ASKLQAQKQSSAALS 488  
 DB 613 MFEKGEWGLLPGNACKSTTSMISSLIQPTSGDVLLKGGSIHKQSKAIRSLGVVQ 672  
 QY 489 FIAYVDYDCE-----GDVGLDLSTKYRLMDNLPQLCSHLRSDGLQEPQHQHFRQ 542  
 DB 673 EIAYVHDLTARENLAFFKRYGLKGEELKLR--MESTLQV-----GLEE-----RQN 718  
 QY 543 SRNRYFRSGRSLYVAICNHQ---FIDEPE 571  
 DB 719 DRYHTSGGMRRLNIAVALLHEPELIIMDEP 750

RESULT 11

Q60669 PRELIMINARY; PRT; 938 AA.  
 ID Q60669  
 AC Q60669;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01; Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21; Last annotation update)  
 DE Protein kinase (Fragment).  
 GN EPHB3.  
 GN MUS musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95200798; PubMed=7893599;  
 RA Ruiz J.C., Conlon F.L., Robertson E.J.;  
 RT "Identification of novel protein kinases expressed in the myocardium  
 RT of the developing mouse heart."  
 RL Mech. Dev. 48:153-164(1994).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 DR EMBL; U11493; AAA67925.1;  
 DR HSP; P29323; 1BAF.  
 DR MGD; MGI:104770; Ephb3.  
 DR InterPro; IPR001090; Ephrin\_receptor.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR003962; FNIII\_repeat.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR001660; SAM.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR001426; Ykase\_receptorV.  
 DR Pfam; PF01404; EPH\_lbd; 1.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR ProDom; PD001495; Ephrin\_receptor; 1.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V1; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V2; 1.  
 KW Glycoprotein; Kinase; Phosphorylation; Receptor; Repeat;  
 KW Transmembrane; Tyrosine-protein kinase.  
 FT NON\_TER  
 FT SEQUENCE 938 AA; 103997 MW; 8D128C46F19E73F CRC64;

Query Match 2.94; Score 115.5; DB 11; Length 938;  
 Best Local Similarity 19.44; Pred. No. 0.33;  
 Matches 160; Conservative 120; Mismatches 285; Indels 259; Gaps 45;

QY 9 SVFTVNAACL-NGSOLAVA-----AGGSGR---ARGADTCGHRMKAARPLRC----- 52  
 DB 170 SLVIAPRACIANAVEVSLKLYCNGDGMVPGACTCATCHEPAKESCRACPPGSY 229  
 QY 53 VANEGVGA-----SRNSG-----LYNITFKYDN-----CITYLNVPVKHVIADAQ 93  
 DB 230 KAKQEGGPGCLPPNSRTTSPAASICTCHNHYRADSDSADSACTTRKSP--PROVISNV- 287  
 QY 94 NITISQACHQDVAVTILWS--PGALGTEFLKGRVILELK--SEG-----ROCOQLIL 144  
 DB 288 -----NETSILEWSEPRDLGGRDDLLYNVICKKRCGSSGAGGATPCSRCDNVE 337  
 QY 145 KDPKQLNSFKRTGHSQPFLLNKKFETDYKVVVPPPSIKNESNTHYFFFRTRACDLLOQ 204  
 DB 338 FVPRQGLTERRVHIS-----HLIAHTRYTFEQAVNGVSGKSLPPRYAAVNTITNQAA 392  
 QY 205 PDLACKPFWKPRNLNISQHSQMSQVSDHAPNFGFFRYLVHKLKHEGPF-KRRTCKQ 263

DB 393 PSEY-----PTLHSHSTSGSLTSLWAPPRPNG---VILDYENKY---PEKSKAIAS 439  
QY 264 BOTTETTSCLQWSP-GDYIIELVDDNTTRKV-----MHYALKPVHSPWAGPIRAVA 316  
DB 440 TVTSQKNSVOLDQDARYVQV-----RARTVAGYQYTHPAEFTTSESGSAQOLO 494  
QY 317 ITVPLVVISAF-----TLFTVCKRKOENIYSHLDESSSESTYTAALPRERLRP 368  
DB 495 BQLPLVGSVAGFVFMVVVVVIALVCLRKORH-----GPDAEYTEKL-QOYIAP 543  
QY 369 RPVFLCYSSKQGNHNNVQCFAYFLQDFC-GCEVALDWEDEFSLCREGQREWIQIH 427  
DB 544 GMKVTDIPFTYEDPN-EAVREFAKEIDVSCVKEEVIGAGEVCR-----589  
QY 428 ESQIIVVCSGKMKYFVDKNTKHKGGGSGGKGELEFLVSAI-----AEKLRQAKQSS 483  
DB 590-----GRUKLGRREVF-VAIKTLKVGYYTERORRDLSEA 623  
QY 484 AALSKEFTANTDYSCGDPVGLDLS---TKYR-----LMDNLPQLGSHLSRDHGLQ 533  
DB 624 SNMGOF-----DHPNIIRLEGVYTKSRPVMILTEFMENC-ALDSFLRLND---667  
QY 534 EPGQHT-----ROGSRNRY-FRSKSGSLAV---AIC-----NMHOFIDE 569  
DB 668---GOFTYQIVGLMRLGIAGMKYILSEMYVIRDLAARNILVNSLVCKVSDGLSRFLED 725  
QY 570 EPDMFEKOF-----VPFH---PPLRYREPVLKEDS-----GLVLDNVCKPGPE 612  
DB 726 DPS---DPTTYSLSGKIPRIWTAPEFIAYR-----KFDASDVMSYGIWMEVNS---773  
QY 613 SDFCLKVEAAVLGATGPADSOHESQHGGLDQGEARALDGSAAQLOPLLTHTVKGASPSDM 672  
DB 774-----YGEQPYWNSNODDINAVEQDYRLPPMDCPYALHQLMASCWVRDRLR 822  
QY 673 PRDSGIYD-----SSVPSELSLPLMEGLSTDOT 701  
DB 823 PRFSOIVNTLDKLRNAASLKVTASAPSG-MSQFLDRTVPDYT 865

RESULT 12  
Q99754  
ID Q99754 PRELIMINARY: PRT: 549 AA.  
AC Q99754:  
DT 01-MAY-1997 (T-EMBLrel. 03, Created)  
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)  
DE 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
DE 68 kDa type I phosphatidylinositol-4-phosphate 5-kinase alpha (BC 2.7.1.68).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
RX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97115834; PubMed=8955136;  
RA Loijens J.C., Anderson R.A.;  
RT "Type I phosphatidylinositol-4-phosphate 5-kinases are distinct members of this novel lipid kinase family";  
RL J. Biol. Chem. 271:32937-32943(1996).  
DR EMBL: U78575; AAC50910.1;  
DR InterPro: IPR002498; PIP5K.  
DR Pfam: PF01504; PIP5K; 1.  
DR SMART: SM00330; PIP5K; 1.  
DR Kinase; transferase.  
KW KINASE; transferase.  
SQ SEQUENCE 549 AA; 61186 MW; 7CD48BFEL75564A0 CRC64;

Query Match  
Best Local Similarity 18.1%; Pred. NO. 0.27;  
Matches 121; Conservative 96; Mismatches 213; Indels 237; Gaps 32;

QY 114 PCAGIEFLK-GFNVILEELKSGRCOCQOLIKDKPKQLNSFKTKCHESOPFLNKKFTD 172  
DB 41 PYASGMPKIKGHSVDSSGCTTKYTKTSALKGAIGIPTHVGLSTKPERDVLMODF 100

QY 173 YFVVVPPPS---LKNESYHPFFTRACDILLQPNLACKPFWKPRNINISQHSMD 228  
DB 101 YVVESIFFPSEGSNTTPAHYNDPRKTYA-----130  
QY 229 QVSDHAPNFCFR---FFY-----LHYLKHGEGPKKCKQKQOTT 267  
DB 131 PVAFRTFRELFRDDDTLYSLCSEPLIELCSGASGLFT-VSSDDEFIITVQHEAE 189  
QY 268-ETTSCLLQWSPGDYIIELVDDNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327  
DB 190---FLOKLLPGYYM---NLQN-----PRTLLPKF 213  
QY 328 ATLFTVCKRKO-----QENIYSHLDESSSESTYTAALPRERLRPRKPVLCYS 377  
DB 214 YGLYCVQAGKRIIVVMNLLPRSVTMHKKYDLKSTYKRRASOKEREKPLP-----T 267  
QY 378 SKDQGNHNVQCFAYFLQDF-CCCEVALDWEDEFSLCREGQREWIO---KIHESOFII 433  
DB 268 FKD-----LDLQDIPDGLFLDADMYN--ALCKTLQDCLVLOSKFIINDYSLM 314  
QY 434 VW-----CSGMYFVDKKNTKHKGGGSGGKGELEFLVAVSAIAEKLRQ-----477  
DB 315 SIHIDBAOREPLSSETOYSVOTR-----RPAQKALYSTAMESIOGEARRGGTMET 366  
QY 478-----AKQSSAALSKFTIANTDYSCGDPVGLDLSLTKYRLMDNLPQLCSHL-HSR 528  
DB 367 DDMGIGIPARNKGBRLLLYI-----GIIDILQSTYFVKKLEHSHKALVHDG 413  
QY 529 DH-GLAEPQGHTRQGSRRNRYFRSKSGSLYVAICNHQFIDEPEWFKQVFPFHPPLR 587  
DB 414 DTVSVRPGFYAERFOR-----FMCN-----TVFKK--IPLKPSPK 448  
QY 588 YREPVLEKDSGLVLDNVCKPGSPDCLKVEAAVLGATGPADSOHESQHGGLDQDEA 647  
DB 449-----KFRSG---SSFSRAGSGNSCTYQPSVSG-----EHRQAQ-----481  
QY 648 RPAIDGSAALQPLHTVKGASPSDMRDSGIYD-----SSVPSELSLPLMEGLSTDOTET 703  
DB 482---VTTKAEVFCVH---LGRPDVLQPTTLEISSESGSIPDPSPFS-PLV-GETLQMLTT 533  
QY 704 SSLTESV 710  
DB 534 STTLEKL 540

RESULT 13  
Q9H460  
ID Q9H460 PRELIMINARY: PRT: 348 AA.  
AC Q9H460:  
DT 01-MAR-2001 (T-EMBLrel. 16, Created)  
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
DE BA425A6.2 (Similar to connexin) (Fragment).  
GN BA425A6.2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
RX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Heath P.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL121749; CAC10186.1;  
DR InterPro: IPR000500; Connexin.  
DR Pfam: PF00029; connexin; 1.  
DR PRINTS: PR00206; CONNEXIN.  
DR SMART: SM00037; CNX; 1.  
DR PROSITE: PS00407; CONNEXINS\_1; 1.  
DR PROSITE: PS00408; CONNEXINS\_2; 1.  
FT NONTER 1  
SQ SEQUENCE 348 AA; 37805 MW; 07EB6478067F8995 CRC64;

Query Match 2.8%; Score 111.5; DB 4; Length 348;  
 Best Local Similarity 28.9%; Pred. No. 0.17;  
 Matches 43; Conservative 25; Mismatches 56; Indels 25; Gaps 8;

QY 600 LVNDVNC-----KPGPESDFCLKVEAAVLGATGAPDASHQSHGGLDQDGEARPAL 651  
 DB 189 LGLADLVCSLRRRRRRPPPTSPSIRKQS---GASGAGRRRTDEGGREEG--APAP 243

QY 652 DGSAAQLPLHTVKAGSDMPDGGIYDSSVP---SSELSPLMEGLSTDTQTSSUTE 708  
 DB 244 PGARA-----GGGAGSPRTSRVSG--HTKIPDESEVTSSASEKLGR-OPGRPHRE 295

QY 709 SVSSSGLG-EEEPALPSKLLSSGCKA 736  
 DB 296 AADPRGSGSEEQPSAAPSRLAAPPSCSS 324

RESULT 14  
 Q96KN9 ID Q96KN9 PRELIMINARY; PRT; 370 AA.  
 AC Q96KN9;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE: Connexin40.1.  
 GN CX40.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Eiberger J., Seehi G., Willecke K.;  
 RT "Structural and functional diversity of connexin genes in the mouse  
 RT submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AJ414564; CAC93846.1; -  
 DR InterPro; IPR000500; Connexin.  
 DR Pfam; PF00029; connexin; 1.  
 DR PROSITE; PS00407; CONNEXINS\_1; UNKNOWN.1.  
 DR PROSITE; PS00408; CONNEXINS\_2; UNKNOWN.1.  
 SQ SEQUENCE 370 AA; 40140 MW; CD49F31743A7FC2 CRC64;

Query Match 2.8%; Score 111.5; DB 4; Length 370;  
 Best Local Similarity 28.9%; Pred. No. 0.18;  
 Matches 43; Conservative 25; Mismatches 56; Indels 25; Gaps 8;

QY 600 LVNDVNC-----KPGPESDFCLKVEAAVLGATGAPDASHQSHGGLDQDGEARPAL 651  
 DB 211 LGLADLVCSLRRRRRRPPPTSPSIRKQS---GASGAGRRRTDEGGREEG--APAP 265

QY 652 DGSAAQLPLHTVKAGSDMPDGGIYDSSVP---SSELSPLMEGLSTDTQTSSUTE 708  
 DB 266 PGARA-----GGGAGSPRTSRVSG--HTKIPDESEVTSSASEKLGR-OPGRPHRE 317

QY 709 SVSSSGLG-EEEPALPSKLLSSGCKA 736  
 DB 318 AADPRGSGSEEQPSAAPSRLAAPPSCSS 346

RESULT 15  
 Q9NTU6 ID Q9NTU6 PRELIMINARY; PRT; 428 AA.  
 AC Q9NTU6;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Hypothetical 45.4 kDa protein.  
 GN DIFZP434P211.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;

SEQUENCE FROM N.A.  
 TISSUE=TESTIS;  
 MEDLINE=21154917; PubMed=11230166;  
 RA Wiemann S., Wall B., Wellenreuther R., Gassenhuber J., Glassl S.,  
 RA Ausorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,  
 RA Tauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,  
 RA Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,  
 RA Wambutt R., Korn B., Klein M., Poustka A.;  
 RT "Towards a Catalog of Human Genes and Proteins: Sequencing and  
 RT Analysis of 500 Novel Complete Protein Coding Human cDNAs";  
 RL Genome Res. 11:422-435(2001)  
 DR EMBL; AL117401; CAB55902.2;  
 KW Hypothetical protein.  
 SQ SEQUENCE 428 AA; 45443 MW; FA75BAC1A3FDB3EE CRC64;

Query Match 2.7%; Score 110; DB 4; Length 428;  
 Best Local Similarity 23.5%; Pred. No. 0.31;  
 Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

QY 474 KLRQAKQSS-SAALSKEIATVFYDSCGSDYVPGI-----LDLSTYRLMDLQ 520  
 DB 103 RYNTQTSWTSSCTNRNAISSYSSSTGGLPGLKRRGPPASSHCQLTLSSTKTVSEDRPQ 162

QY 521 LCSHLHSRDHGLQZ--PGQHTROGSRNRYFRSKGRSLYVAICNMHQFIDEEPWFQKF 578  
 DB 163 AVSSGHTQCEKAADIAPGQTLT--LRNDSSTSEASRP-----STHKF---PLLPRRG 210

QY 579 VPPH-PPPL-----RYREPVLKFDGSLVNDVM--CKPGPESDFCLKVEAA 622  
 DB 211 EPLMLPPPLELGYRTVEDLDREKAAAFQINSALQVEDKAISSDGRPSRPSH---TLSSL 267

QY 623 VLATG-PADSHESQHGGLDQDGEARPALDGSAAQLPLHTVKAGSDMP-----RD 675  
 DB 268 ATGASGLPAVSKAPS---NDAAQOETHKSDQCLGLDPLASA--AGVETAPMSGKKHRP 321

QY 676 SG-IYDSSVPSSELSPLMEGLSTDTQTSSLTVESVSSSGLGEEEPALPSKLLSSG 732  
 DB 322 PGPFLSSDP-----LPATSSDSQDSQAQVTSLI-----PAPFAASMDAG 361

Search completed: May 6, 2003, 13:44:47  
 Job time : 103 sec



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OM protein - protein search, using sw model

Run on: May 6, 2003, 13:41:56 ; Search time 30 Seconds  
(without alignments)  
738,515 Million cell updates/sec

Title: US-09-912-157-2  
Perfect score: 4013  
Sequence: 1 MAPWLQCSVFTYNACLG.....CKADLCGRSYTDELHVAAPL 753

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2.6/ptodata/1/iaa/5A.COMB.pdp:\*
- 2: /cgn2.6/ptodata/1/iaa/5B.COMB.pdp:\*
- 3: /cgn2.6/ptodata/1/iaa/6A.COMB.pdp:\*
- 4: /cgn2.6/ptodata/1/iaa/6B.COMB.pdp:\*
- 5: /cgn2.6/ptodata/1/iaa/PCIRUS.COMB.pdp:\*
- 6: /cgn2.6/ptodata/1/iaa/backfiles1.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	312	7.8	866	2	US-08-620-694A-10
2	312	7.8	866	3	US-09-022-255-10
3	312	7.8	866	3	US-09-022-696-10
4	312	7.8	866	3	US-08-978-773-4
5	312	7.8	866	3	US-09-022-253-10
6	312	7.8	866	3	US-09-022-260-10
7	312	7.8	866	4	US-09-022-259-10
8	312	7.8	866	4	US-09-022-257-10
9	306	7.6	864	2	US-08-620-694A-2
10	306	7.6	864	3	US-09-022-255-2
11	306	7.6	864	3	US-09-022-696-2
12	306	7.6	864	3	US-08-978-773-2
13	306	7.6	864	3	US-09-022-253-2
14	306	7.6	864	3	US-09-022-260-2
15	306	7.6	864	4	US-09-022-259-2
16	306	7.6	864	4	US-09-022-257-2
17	116.5	2.9	993	1	US-08-348-143-1
18	116.5	2.9	993	1	US-08-571-785-1
19	116.5	2.9	993	4	US-09-192-435-1
20	116.5	2.9	993	4	US-09-558-340-1
21	115	2.9	998	2	US-08-449-645A-20
22	115	2.9	998	2	US-08-702-367A-20
23	113.5	2.8	617	4	US-09-188-930-303
24	99	2.5	595	1	US-08-468-036-3
25	99	2.5	595	2	US-08-376-843-3
26	97	2.4	951	1	US-08-162-809-2
27					

28	96	2.4	424	3	US-09-209-668-17	Sequence 17, Appl
29	96	2.4	424	5	PCT-US94-12913A-18	Sequence 18, Appl
30	96	2.4	984	2	US-08-673-789-6	Sequence 6, Appl
31	95	2.4	933	4	US-08-764-870-14	Sequence 14, Appl
32	95	2.4	933	4	US-08-980-115-14	Sequence 14, Appl
33	94	2.3	424	4	US-09-025-580-32	Sequence 32, Appl
34	94	2.3	3224	2	US-08-705-660-34	Sequence 34, Appl
35	94	2.3	3224	3	US-08-989-045-34	Sequence 34, Appl
36	93.5	2.3	828	2	US-08-993-228-21	Sequence 21, Appl
37	92.5	2.3	347	4	US-08-630-915A-32	Sequence 32, Appl
38	92.5	2.3	2308	1	US-08-015-973-1	Sequence 1, Appl
39	92.5	2.3	2308	2	US-08-448-164-1	Sequence 2, Appl
40	92.5	2.3	2308	4	US-08-081-929-2	Sequence 2, Appl
41	92.5	2.3	2314	4	US-09-816-703A-2	Sequence 2, Appl
42	91.5	2.3	1838	4	US-09-120-665-2	Sequence 2, Appl
43	90.5	2.3	483	2	US-08-583-562B-12	Sequence 12, Appl
44	90.5	2.3	483	2	US-08-779-113-12	Sequence 12, Appl
45	90.5	2.3	857	2	US-08-779-113-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-620-694A-10  
Sequence 10, Application US/08620694A  
Patent No. 5869286  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION NUMBER: US/08/620,694A  
FILING DATE: 21 MARCH 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-620-694A-10

Query Match 7.8% Score 312; DB 2; Length 866;



Best Local Similarity 23.1%; Pred. No. 1.9e-23;  
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITFYDNC--TTLNPGKRVIAADQNIT-----ISOYACHDQ-----VAVTILMS 113  
DB 49 NCTVKNSTCLDSDWIHP-----RNLTPSSPKDLQIQLHFAHTQOGLFPVAHLEWT 99

QY 114 -PGALGIEFLKGFVILEELKSGQCQQLILKDPKQNSFKRGMESQPLNKKFETD 172  
DB 100 LQTDASILYLEGAELSVQLNTNERLCVR--FEELSKLRHHRWRFTFSHFV--VDPDQE 156

QY 173 YFVKV--VFPISIKNESYHFFFRTRACDILLQPDNLACK-----PFMKPRNL----- 219  
DB 157 YEVTVHLLPRIPDGDPNHQSKNELVPDCEHAKMVTTPCMSGSLMDP--NITVETLEAH 501

QY 220 -----NISQHSQDMOVSFDAHPNFGFRFFYLHYKLMEGPFKEKTCQBOETTET 270  
DB 216 QLRVSTLANESTHYQILLTSPFMENHSCFEHMH--HIPAPRPEEFHQRSVNLTLRNLK 274

QY 271 SCQLQNVSPGDIIEELVDDT--NTRKVMHYALKPVHSPWAGPIRAVAITPVLVVISAF 327  
DB 275 GCCRHOVQIQPFSSCLNCLRHSAIVSCPEMDTPEDIPDYAPLWVYFETIGISILLVG 334

QY 328 ATFLTYMCRKKQENIYSHLDESESSYTTAALPRERLRPR-----KVFLCYSSKQOGN 383  
DB 335 SVILLIVCMWRLAGPGS---EKYSDDTKYTDLGPAADLIPPLPKRVKVIYSA--DHPL 390

QY 384 HMNVVQCFAYFLQDFCCGEVALDLWEDFSLCREGQREWV---IQKHESQFIIVVCSKG 439  
DB 391 YDVLVLEFAQFLITACGTEVALDLLEQAISEAGVMTVWGQKQENVESKIIIVLCSRG 450

QY 440 MYFVYDKNKKHKGKGG-----RSGSGKGEFLVAVSAIAEKLQAKQSSAALSXFIA 491  
DB 451 TR-----AKWQALLRGAPVRLCRDCHGKPVGDLFTAAMNMLPDKR-----PACFCGTIVV 501

QY 492 VTF--DYSCGDPVGLDLSKYRLMDNLPCLSHLSDRGLQEPGQHTROG--SRNRYF 548  
DB 502 CYFSEVSCDGDVPLDGAAPRYPLMDRFEV--YFRIQDLEMFQGRHVRGELSGDNIL 559

QY 549 RSKSGSLVAICNMHQFIDEEPWF-----KQFVFPHPPLRYREPVLEKFDGSL 600  
DB 560 RSPGRLRAALDRFMQVRCDFWPCFENLYSADDDAPSILDEEV--FEEPLLP--GTGI 617

QY 601 VLMDVMCKPGSPDCLKVEAAVLGATGPADSOHE-----SOHGG 640  
DB 618 VKRAPLVRE--PGSOACLAIDPLVGEEGAVALKLEPHLQPCQAPQPLHTLVLAEEGA 676

QY 641 LDQGEARALDGA--ALQ-----PLIHTVKGSPDMPRDSGIYDSSVPSSELSLP 691  
DB 677 LVAAVEPGLADGAARLALAGEAGEACPLLGSPGAG-----RNSVLP---LPVDPEDSP 727

QY 692 LMGLSLTDQTTSTTESVSSSGSGEPEPPALPSKLLSSGSKADLGC 740  
DB 728 L--GSSTPMSPDLPEDVR-----EHLGLMLSLFEQSLSCQAQGC 768

## RESULT 2

US-09-022-255-10  
; Sequence 10, Application US/09022255  
; Patent No. 6072033  
; GENERAL INFORMATION:  
; APPLICANT: Yao, Zhengbin  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Fanslow, William  
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,255  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/620,694  
FILING DATE: 21 MARCH 1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO.: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-255-10

Query Match 7.8%; Score 312; DB 3; Length 866;  
Best Local Similarity 23.1%; Pred. No. 1.9e-23;

Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITFYDNC--TTLNPGKRVIAADQNIT-----ISOYACHDQ-----VAVTILMS 113  
DB 49 NCTVKNSTCLDSDWIHP-----RNLTPSSPKDLQIQLHFAHTQOGLFPVAHLEWT 99

QY 114 -PGALGIEFLKGFVILEELKSGQCQQLILKDPKQNSFKRGMESQPLNKKFETD 172  
DB 100 LQTDASILYLEGAELSVQLNTNERLCVR--FEELSKLRHHRWRFTFSHFV--VDPDQE 156

QY 173 YFVKV--VFPISIKNESYHFFFRTRACDILLQPDNLACK-----PFMKPRNL----- 219  
DB 157 YEVTVHLLPRIPDGDPNHQSKNELVPDCEHAKMVTTPCMSGSLMDP--NITVETLEAH 501

QY 220 -----NISQHSQDMOVSFDAHPNFGFRFFYLHYKLMEGPFKEKTCQBOETTET 270  
DB 216 QLRVSTLANESTHYQILLTSPFMENHSCFEHMH--HIPAPRPEEFHQRSVNLTLRNLK 274

QY 271 SCQLQNVSPGDIIEELVDDT--NTRKVMHYALKPVHSPWAGPIRAVAITPVLVVISAF 327  
DB 275 GCCRHOVQIQPFSSCLNCLRHSAIVSCPEMDTPEDIPDYAPLWVYFETIGISILLVG 334

QY 328 ATFLTYMCRKKQENIYSHLDESESSYTTAALPRERLRPR-----KVFLCYSSKQOGN 383  
DB 335 SVILLIVCMWRLAGPGS---EKYSDDTKYTDLGPAADLIPPLPKRVKVIYSA--DHPL 390

QY 384 HMNVVQCFAYFLQDFCCGEVALDLWEDFSLCREGQREWV---IQKHESQFIIVVCSKG 439  
DB 391 YDVLVLEFAQFLITACGTEVALDLLEQAISEAGVMTVWGQKQENVESKIIIVLCSRG 450

QY 440 MYFVYDKNKKHKGKGG-----RSGSGKGEFLVAVSAIAEKLQAKQSSAALSXFIA 491  
DB 451 TR-----AKWQALLRGAPVRLCRDCHGKPVGDLFTAAMNMLPDKR-----PACFCGTIVV 501

QY 492 VTF--DYSCGDPVGLDLSKYRLMDNLPCLSHLSDRGLQEPGQHTROG--SRNRYF 548  
DB 502 CYFSEVSCDGDVPLDGAAPRYPLMDRFEV--YFRIQDLEMFQGRHVRGELSGDNIL 559

QY 549 RSKSGSLVAICNMHQFIDEEPWF-----KQFVFPHPPLRYREPVLEKFDGSL 600

Db 560 RSPGRLRAALDRFQWRCDFNFECECNLYSADDDAPSLDEY-FEELPLP-617  
 QY 601 VLNDVCKPGPESDFCLKVEAIVLGATGADSOHE-----SQHGG-640  
 Db 618 VKRAPLVRE-PCSQACLAIDPLVGEGBAIVAKLEPHLQPGQAPQPLHTLVLAEEGA 676  
 QY 641 LDQGEARPALDGA---ALQ-----PLHTVYKAGSPDMRDSGIYDSSVPSSELSLP 691  
 Db 677 LVAAVEGPLADGAARALAGGEACPLLASPGAG-----RNSVLF---LPVDPEDSP 727  
 QY 692 LMEGSLTDOTSTSLTESVSSSGLEGEPPALPSKLLSSGSKADLGC 740  
 Db 728 L-GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

## RESULT 3

US-09-022-696-10  
 ; Sequence 10, Application US/09022696  
 ; Patent No. 6072037

## GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
 APPLICANT: Spriggs, Melanie  
 APPLICANT: Fanslow, William  
 TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17,  
 NUMBER OF SEQUENCES: 10

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Power Macintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/022,696

## FILING DATE:

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/620,694  
 FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/410,535  
 FILING DATE: 23 MARCH 1995

## ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)

## INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 866 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-022-696-10

Query Match: 7.8%; Score 312; DB 3; Length 866;

Best Local Similarity: 23.1%; Pred. No. 1.9e-23;

Matches: 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITKYNDC---TTLNVPKGVHVAQNT-----ISOYACHQD-----VAVTILWS 113

Db 49 NCTVKNSTLDDSWIHP-----RNLTPSPKDLQIQIHFAHTQGDLPFAHIEWT 99

QY 114 PGALGIEFLKGRVILEELKSEGROCOOLILKDPKOLNSSFRTKMGESQPEFLNNKFFTD 172  
 Db 100 LQTDASLILEGAEILSVLQATNRELQVR--FEFLSKLRHHHRRWFTFSHEV-YDPOE 156  
 QY 173 YFVTV--VPPSPKSNESNHPFFTRACDILLQDPMACK---PFWKPRNL-----219  
 Db 157 YEYVHLHPKPIPDGPNHQSKNFLVPCDEHARKVITPCMSGSLMDP-NITVETLEAH 215  
 QY 220 -----NISQSGDMQVSDHAPHNFGFRFFLYHLKHEGPKFKTKCQEQTTETT 270  
 Db 216 QLRSVFTLNWSETHYQILLTSPHMEISCFEEMH-HIPAPREEEPHORSNTLRLNLK 274  
 QY 271 SCLIONVSPGDIYIELVDT---NTRKVMHYALKPVHSPWAOPIRAVAITVPLVVISAF 327  
 Db 275 GCRHQVQIQPFSSCINDLHRSATVSCPEMDTPEPIFYMLPVWYFWTIGISILLVG 334  
 QY 328 ATLFTVMCRKQOENIYSHLDESESESTYTAALPRELRPRP-----KVFLCYSSKQGN 383  
 Db 335 SVILLIYVMTWRLAGPS---EKYSDDTKYTDGLPAADLIPPLKPKRWIYISA-DHPL 390  
 QY 384 HMVVOCFAYFLQDFGCEVALDWEFSLCREGEWV----IQKIHESQFIIVVCSKG 439  
 Db 391 YDVVLKFAQFLITAGCTEVALDLEQAISEAGVMTWGRQKQEMVESNKIIVLCRSG 450  
 QY 440 HKYEVDRKNTKHKGG-----RSGSGELFLVAVSAIAEKLRQAKOSSAALSKEIA 491  
 Db 451 TR---AKWQALIGRGAIVRLCDHGRKPVGDLFTAAHMLPDKR-----PACFTGVV 501  
 QY 492 VYF-DYSCGDVPGILDITKYRLMDNLPLQCSHLHSRDHGLQEPQOHTROG--SRRNYF 548  
 Db 502 CYFSEVSCDGDVPLFGAARPTPLADREEV--YFIQDLENFQPGRMHRYGELSGDYL 559  
 QY 549 RSKSGSLYVACNMHQFIDEEDPWE-----KQFVFPHPPLRYEPVLEKFDGSL 600  
 Db 560 RSPGRLRAALDRFQWRCDFNFECECNLYSADDDAPSLDEY-FEELPLP-617  
 QY 601 VLNDVCKPGPESDFCLKVEAIVLGATGADSOHE-----SQHGG-640  
 Db 618 VKRAPLVRE-PCSQACLAIDPLVGEGBAIVAKLEPHLQPGQAPQPLHTLVLAEEGA 676  
 QY 641 LDQGEARPALDGA---ALQ-----PLHTVYKAGSPDMRDSGIYDSSVPSSELSLP 691  
 Db 677 LVAAVEGPLADGAARALAGGEACPLLASPGAG-----RNSVLF---LPVDPEDSP 727  
 QY 692 LMEGSLTDOTSTSLTESVSSSGLEGEPPALPSKLLSSGSKADLGC 740  
 Db 728 L-GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

## RESULT 4

US-08-978-773-4  
 ; Sequence 4, Application US/08978773  
 ; Patent No. 6083906

## GENERAL INFORMATION:

APPLICANT: Troutt, Anthony  
 TITLE OF INVENTION: Method of Regulating Nitric Oxide Production  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple PowerMacintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/978,773  
 FILING DATE:  
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 60/052,525  
FILING DATE: 27 NOVEMBER 1996  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2623-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 866 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-978-773-4

Query Match 7.8%; Score 312; DB 3; Length 866;  
Best Local Similarity 23.1%; Pred. No. 1.9e-23;  
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITEKYDNC--TTLNPGVKHVIADQNIT-----ISQYACHDQ-----VAVTILWS 113  
DB 49 NCTVNSTCLDSDSWHP-----RNUTPSSPKDLQQLHFAHTQGDLPFVAHIEWT 99  
QY 114 -PGALGIEFLKGRVILEELKSEGRQCOQLILKDPKLNSSFKRTGMSOPFLNMKFETD 172  
DB 100 LOTDASILYLEGAEISVLQNTNERLCVR--FEFLSKLHHHRWRFTFSHFV-VDPDQE 156  
QY 173 YFVKV--VFPISIKNESYHFFETRACDILLQPDNLACK--PFWKPRNL----- 219  
DB 157 YEYVHHLPRIPDGDPHQSKNLFVPCDEHARKVITPCSSGSLWDP-NITVETLEAH 215  
QY 220 -----NISQHSQDMQVSFDHAPNFGFRFFLYHLKLBHGGPFKRKTCQEQTTT 270  
DB 216 QLRVSTFLWNETHYQILLTSFPHENHSCFPHMH-HIPAPRPEEFHQRNSVTLRLNK 274  
QY 271 SCILQNVSPGDIIEELVDIT---NTTRKVMHVALKPVSPWAGPIRAVAITVPLVISA 327  
DB 275 GCRHQVQIOPFSSCLNDCLRHSAITVSCPEMDTPEIPDYMPLWYTFITGISLLVG 334  
QY 328 ATLFTYCKKQOENIYSHLDEESSSTYTAALPRERLRPP-----KVLCTSSKDGQN 383  
DB 335 SVILLIVCTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKRWIISA-DHPL 390  
QY 384 HNNVQCFAYFLQDCGCEVALDIEDFSLCREGQREW---IOKIHESOFITVVCCKG 439  
DB 391 YVDVVLKFAQLLTACGTEVALDLEQAISEAGVMTWVGOKOBWESNSKIIVLCRSG 450  
QY 440 MYFVDDKNYKHGGG-----RSGSGELFLVAVSAIAEKLQAKQSSAALSKEFTA 491  
DB 451 TR-----AKWQALLGKAPVRLRCDHGPVGDLPFTAMNMLIPFKR-----PACFGTYV 501  
QY 492 VTF-DYSCGDPVGLDSTKYLRLMNLPLQCSHLHSDHGLQEPQHTROG--SRNRYF 548  
DB 502 CYFSEVSCDGDVDPDLFGAARPYLMORFEV--YFRIODLEMFQGRHVRGELSGDNYL 559  
QY 549 RSKSGRLVATCNHOFIDEEPWFPE-----KQFVPEHPPLRYREPVELEKEDSGL 600  
DB 560 RSPGQRLRALDRFROHQVRCDFWECENLYSADDDAPSLDEEV-FEELPLPP-GTGI 617  
QY 601 VLNDVCKPGPSPDFCLKVEAVLIGATGPADSGHE-----SQHGG-640  
DB 618 YKRAPLVRE-PCGQACLAIDPLVGEEGAAGAAVLEPHLQPGQAPAPQPLTLVLAEEGA 676  
QY 641 LDQDGARPALDGA--ALQ-----PLIHTVKAGSDMPROSGIYDSSVSSSELSLP 691  
DB 677 LVAAVEKPLADGANVRLALAGEACEACPLIGSPGAC-----RNSVLE---LPVDPEDSP 727  
QY 692 LMEGLSTOOTETSSITSEVSSSSGLGEEPPALPKLLSSGSKRADLGC-740

DB 728 L--GSSTPMASPDILLPEDVR-----EHLEGLMLSLFRQSLSCQAOGGC 768

## RESULT 5:

US-09-022-253-10  
Sequence 10; Application US/09022253  
Patent No.: 6096305

## GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,253

## FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/620,694

FILING DATE: 21-MARCH-1996

APPLICATION NUMBER: USSN 08/538,765

FILING DATE: 7 AUGUST 1995

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:

## SEQUENCE CHARACTERISTICS:

LENGTH: 866 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-022-253-10

## Query Match

7.8%; Score 312; DB 3; Length 866;

Best Local Similarity 23.1%; Pred. No. 1.9e-23;

Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 69 NITEKYDNC--TTLNPGVKHVIADQNIT-----ISQYACHDQ-----VAVTILWS 113  
DB 49 NCTVNSTCLDSDSWHP-----RNUTPSSPKDLQQLHFAHTQGDLPFVAHIEWT 99  
QY 114 -PGALGIEFLKGRVILEELKSEGRQCOQLILKDPKLNSSFKRTGMSOPFLNMKFETD 172  
DB 100 LOTDASILYLEGAEISVLQNTNERLCVR--FEFLSKLHHHRWRFTFSHFV-VDPDQE 156  
QY 173 YFVKV--VFPISIKNESYHFFETRACDILLQPDNLACK--PFWKPRNL----- 219  
DB 157 YEYVHHLPRIPDGDPHQSKNLFVPCDEHARKVITPCSSGSLWDP-NITVETLEAH 215  
QY 220 -----NISQHSQDMQVSFDHAPNFGFRFFLYHLKLBHGGPFKRKTCQEQTTT 270  
DB 216 QLRVSTFLWNETHYQILLTSFPHENHSCFPHMH-HIPAPRPEEFHQRNSVTLRLNK 274

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QY 271 SCLQNVSPGDIYIELVDDT---NTRKVMHVALKPVHSPWAGPIRAVAITVPLVVISAF 327
DB 275 GCRHQVQIQPFSSCLNCLRHSAVSCPMPDTPPIPIYDMLWYNEITGISILLVG 334
QY 328 ATLFVWCKKQKQENIYSHLODESSSYTAALPREKLRPP-----KVFCLYSSKQDN 383
DB 335 SVILLVCMWRLAGPGS---EKYSDDTYTDLGPAADLPPPLPKPKWIIYSA-DHPL 390
QY 384 HMYVQCFAYFLDFCCEVALDWEFSLCREGQEWV---LQKHESQFIIVVCSKG 439
DB 391 YVDVVLKFAQLTACGTEVALDLEEQALSEAGVMTWVGRQKQEMVESKIIIVLC SRG 450
QY 440 MKYFVCKKYNKHKGG-----RSGKGELFVAVSAIAERLQAKQSSAALSFKFIA 491
DB 451 TR-----AKWQALLGRCAPVRLRCDHGKPVGDLPFTAMNNILPDFKR-----PACFGTVV 501
QY 492 VYF-DYSCGDPVGLDLSKYRLMDNLPQLCSHLHRDGHGLOEPGQHTROG---SRRYV 548
DB 502 CYFEVSCDGVDPDLFGAAPRYPLMDRFEV---YFRIDLEMFQPGRMHVRGELSGDNYL 559
QY 549 RSKGRSLYVAICNMHOFIDEEPDMFE-----KQVFPHPPLRYREPVLKFDL 600
DB 560 RSPGRQLRAALDRFRDQVRCDFMFCENLYSADDQDAPSLDEEV---FEEPLPP-GTGI 617
QY 601 VLNDVCKPGPESDFCLKVEAAVYLGATGPADSQHE-----SQHGG 640
DB 618 VKRAPLVRE-PGSOACIADPLVGEAGAAVAKLEPHLQPRGQAPQPLHLVLAAE GA 676
QY 641 LDQGEARPALDGA---ALQ-----PLHTVVKAGSPDMRSDGIYSSVPSSELSIP 691
DB 677 LVAAVEPGPLADGAARVRLALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
QY 692 LMEGLSTQDTSTSLTESVSSSGLEGEPPALPSKLLSSGCKADIGC 740
DB 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFQSLSCQAQGGC 768

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## RESULT 6

```

US-09-022-260-10
; Sequence 10, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Blinds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/022,260
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-260-10

```

Query Match 7.8%; Score 312; DB 3; Length 866;

Best Local Similarity 23.1%; Pred. No. 1.9e-23;

Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

```

QY 69 NITKYNDC--TYLNPVCKHVIADAQNT-----ISQYACHDQ-----VAVTILWS 113
DB 49 NCTVKNSTCLDDSWHP-----RNLTPSSPKDLQIQLHFAHTQOGLFPVAHIEMT 99
QY 114 PGALGIEFLKQPRVILELSEKSEGCQOOLIKDPKOLNSFRTKQESQPLNKKFTFD 172
DB 100 LQTDASLILYLEGAEISVLQANTNERLCVR---FEFLSKLRHHRHRRFTFSHEV-VDPQ 156
QY 173 YFVKV--VPPPSIKNSNTHPFFFTTRACDLLLLQDNLACK---PFWKPNL----- 219
DB 157 YEIVTHLPKPIPDGPNHQSNELVPDCEHARKMVTTPCKSSGSLWDP-NITVETLEAH 215
QY 220 -----NISQSGDMQVSTDPHAPNFGFRFFLYLKLKHEGPFRTCKQEQOTTETT 270
DB 216 QLRVSTFLWNESTHYQILLTSEPHNESCFEHMR-HIPAPRPEEFHORSNTVTLRNLK 274
QY 271 SCLQNVSPGDIYIELVDDT---NTRKVMHVALKPVHSPWAGPIRAVAITVPLVVISAF 327
DB 275 GCRHQVQIQPFSSCLNCLRHSAVSCPMPDTPPIPIYDMLWYNEITGISILLVG 334
QY 328 ATLFVWCKKQKQENIYSHLODESSSYTAALPREKLRPP-----KVFCLYSSKQDN 383
DB 335 SVILLVCMWRLAGPGS---EKYSDDTYTDLGPAADLPPPLPKPKWIIYSA-DHPL 390
QY 384 HMYVQCFAYFLDFCCEVALDWEFSLCREGQEWV---LQKHESQFIIVVCSKG 439
DB 391 YVDVVLKFAQLTACGTEVALDLEEQALSEAGVMTWVGRQKQEMVESKIIIVLC SRG 450
QY 440 MKYFVCKKYNKHKGG-----RSGKGELFVAVSAIAERLQAKQSSAALSFKFIA 491
DB 451 TR-----AKWQALLGRCAPVRLRCDHGKPVGDLPFTAMNNILPDFKR-----PACFGTVV 501
QY 492 VYF-DYSCGDPVGLDLSKYRLMDNLPQLCSHLHRDGHGLOEPGQHTROG---SRRYV 548
DB 502 CYFEVSCDGVDPDLFGAAPRYPLMDRFEV---YFRIDLEMFQPGRMHVRGELSGDNYL 559
QY 549 RSKGRSLYVAICNMHOFIDEEPDMFE-----KQVFPHPPLRYREPVLKFDL 600
DB 560 RSPGRQLRAALDRFRDQVRCDFMFCENLYSADDQDAPSLDEEV---FEEPLPP-GTGI 617
QY 601 VLNDVCKPGPESDFCLKVEAAVYLGATGPADSQHE-----SQHGG 640
DB 618 VKRAPLVRE-PGSOACIADPLVGEAGAAVAKLEPHLQPRGQAPQPLHLVLAAE GA 676
QY 641 LDQGEARPALDGA---ALQ-----PLHTVVKAGSPDMRSDGIYSSVPSSELSIP 691
DB 677 LVAAVEPGPLADGAARVRLALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
QY 692 LMEGLSTQDTSTSLTESVSSSGLEGEPPALPSKLLSSGCKADIGC 740
DB 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFQSLSCQAQGGC 768

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RESULT 7

US-09-022-259-10



SEQUENCE CHARACTERISTICS:  
 LENGTH: 866 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-022-257-10

Query Match 7.8%; Score 312; DB 4; Length 866;  
 Best Local Similarity 23.1%; Pred. No. 1.9e-23;  
 Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

69 NITEKYDNC--TTLNPGVGHVADAGNIT-----ISOYACHDQ-----VAVTILWS 113  
 49 NCTVNSCLDDSHHP-----RNLTPSSPKDQIQIAPHAHQDGLFPVAHIEWT 99  
 114--PGALGIEFLKGFVLEELKSGRCQQOILKDKPQNSKFRKMGESOPFLNKKFTD 172  
 100 LQTDASILYLEGAEISVLQNTNERLCVR--FEFLSKLRHHRWRFTSHEV-VDPOE 156  
 173 YEVKY--VPPFSIKNESNYHFFRTRACDILLOPDNLACK---PEFKPRNL----- 219  
 157 YEVTVHLPKPIPDGDPHQSKNFLVPDCEHARKVYTPCMSSGSLMDP-NITVETLEAH 215  
 220-----NISQSGDMQVSDHAPHNFGFRFFLYHYKLLKHEGPPFRKTKOEQTETT 270  
 216 QURVSTLWNESTHYQLTSPHMHNSCFEPMH-HIPAPRPEEPRHRSNVTLLRLNLK 274  
 271 SCLQNSPGDYIELVDOT---NTRKVMYALKPVHSPWAGPIRAVAITPLVVISAF 327  
 275 GCRHVGIOIOPFFSSCLNDCLRHSAVSCPENPDTPPIPDYPLVAVYFITGISILLVG 334  
 328 ATLETVMCRKKQOENIYSHLDESSSTYTAALPRELRPR-----KVELCYSSKDGON 383  
 335 SVILLIVCMWRLAGPS---EKISDTYDGLPADLIPPLPKRKYWIIISA-DHPL 390  
 384 HANVVOCFAYFLQDFGCEVALDLWEDFSLCREGOREWY----IOKIHESQFIIVVCSKG 439  
 391 YDVVLFAFQFLTACGTEVALDLLEQAISEAVMTWVGROKQEMVESNRIIVLCRSG 450  
 440 KRYFDKKNKKHKGKG-----RSGKGELFLVAVSAEKLROAKOSSAALSCKFTA 491  
 451 TR---AKWALLGRGAPVRLRCHGKPVGDLFTAANNMILPDFKR-----PACGCTVYV 501  
 492 YTF-DYSCGDVPCILDSTKYRLMDNLPOLCSHLHSDHGLQEPGQHTROG--SRNYVP 548  
 502 CTFSEVSCDGDVPLFGAAPRYPLMDRFEV--YFRIDOLENFPQGRMHRVGLSGDNYL 559  
 549 RSKSGSLYVAICNMHQFIDEEDWFE-----KQVPFPHPPRLRYREPVLEKFDGSL 600  
 560 RSPGGRQLRAALDRFRDMQVRCPDWFECENLYSADDQADPSLDEEV-FEPLLP-GTGI 617  
 601 VLNDVMCKPGPESDFCLKVAEAVLCATGPADSQHE-----SQHGG 640  
 618 VRAPLVRE-PGSOACLAIDPLVGEGBAAVAKLEPHLQPGCAPQPLETLVLAAEBA 676  
 641 LDQGEARPALDGA---ALQ-----PLLHTVAGSPSDMRDGIYDSSVPSSLSLP 691  
 677 LVAAVEPGLADGAARLALAGEACPLIGSPGAG-----RNSVLF--LPVDPESP 727  
 692 LMEGLSTQDTETSLTESVSSSGLGEPEPALPSKLLSGCKADLGC 740  
 748 L--GSSTPMASPOLLPEDVR-----EHLEGLMISLFEQLSQAQGGC. 768.

## RESULT 9

US-08-620-694A-2

Sequence 2, Application US/08620694A

Patent No. 5869286

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Power Macintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/620,694A  
 FILING DATE: 21 MARCH 1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/538,765  
 FILING DATE: 7 AUGUST 1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/410,535  
 FILING DATE: 23 MARCH 1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)597-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 864 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-620-694A-2

Query Match 7.6%; Score 306; DB 2; Length 864;

Best Local Similarity 22.5%; Pred. No. 8.2e-23;

Matches 169; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

40 GWRM-----KAARPRU-----CVANEGVGPASRNSGLNITFKYDNCITLYNPVKR 86  
 17 GWILLILNVLAPGRASPRLLDPPAPVCAQEGLSCKVENSTCLDSDWIHPKNTLTPSSPKNI 76  
 87 HVIADAQNTISQYACHDQAVT-ILMS-PCALGIEFLKGFVLEELKSGRCQQO--- 141  
 77 YI-----NLSVSTOGEVLVPLVHVEVTLQTDASILILEGAEISVLQNTNERLCVRFQ 131  
 142--LILKDPKOLNSKFRKMGESOPFLNKKFTDYFKVWVPFSPKINESNYHFFRTRAC 199  
 132 LSMLOHRRKWRFSF-----SHFVDPGQYEVTVHHLPKPIPDGDPNHRKSLFVPC 185  
 200 D-----LLLOPDNLACKPFKKPRNLN-----SOH-----GSDMQV 230  
 186 EDKMKMTTSCVSSGSLMDP-NITVETLDTQHLRVDTLWNESTPYQVLLSFSDSENHS 244  
 231 SFD-----HAPHNFGFRFFLYHYKLLKHE---GPFKRTCKOEQTETTSCLL 274  
 245 CFQVVKQIFAPROEERFORANVTFTLSKFHWCCHHHVQVQPF-FSSCLND-----CLR 296  
 275 QNVSPGDIYIELVDOTNTTRKVMYALKPV--HSP-WA-GPIRAVAITPLVVISAFATL 330  
 297 HAVTVCPVI-----SNT-----VPKVADYIPLVNYGLITLAI-----LLVGSVYL 341  
 331 FTWACRRKQOENIYSHLDEESSESTYTAALPRELRPRKPVLCYSSKDGONHNVQC 390  
 342 IICMTWRLSGAQDEKHGDDSKINGILFVADITPPPLRPR-KVMIVISA-DHPLVVEVYLK 399  
 391 FAYFLQDFGCEVALDLWEDFSLCREGOREWVIOK-----IHESQFIIVVCSKGKMYFVK 446

Db 400 FAQFLITACGTEVALDLEQVTSYGVMTWYSROKQEMVESNKKIILCSRG-----TQ 454  
 QY 447: KNYKHGG-----GRSGKGEFLVAVSAIAEKLQAKQSSAALSKEIAVYFDY 496  
 Db 455 AKWAILGMAEPVQLRCDHMKPAGDLFTAAANNMILPDFKR-----PACFGTVVYCFSG 509  
 QY 497: SC-EGDVPGILDSTKYRLMDNLPOLCSHLHSRDHGLQEPQ--HTROGSRNYFYSKSG 553  
 Db 510 ICSEKDVDFLNTSRYPMDREEV--YFRIQDLEMFEPGRMHVRELGDNYLQSPSG 567  
 QY 554 RSLYVAICNMHQFIDBEPDFKQFVFPHP-----PPLR---YREPVLEKFDGLVNDVM 606  
 Db 568 ROLKAVLRFOEMOTOCDFWFERENCLADGDLPSLDEEVEFDPLPP--GGGIVKQOPL 626  
 QY 607: CKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQD-----GEAR 648  
 Db 627 VRELP--SDGCLVYDVCV-----SEESRMALDQPMQRELVAHTLQSNVLPAGQV 677  
 QY 649 PALDGSAAQLPILRTYKAGSPDMP--RDS-----GIYDSSV---PSSELSLPL-----692  
 Db 678 PA---AHVVEPLHLPDGSAAQLPMTEDSEACPLLVQVORNSILCLPVDSDDLPLCSTPM 734  
 QY 693 -----MEGLSTDOTETSLTESVSSSGLGEEPEPALPSKLLSSGCKADLCGRSYTDE 746  
 Db 735 MSPDHLOGDAREQLESMLSVLQOSSLGQPLESNPR-PEVYLE-----GCTPSEEE 784

## RESULT 10

US-09-022-255-2  
 ; Sequence 2, Application US/0902255  
 ; Patent No. 6072033  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yao, Zhengbin  
 ; APPLICANT: Spriggs, Melanie  
 ; APPLICANT: Fauslow, William  
 ; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Power Macintosh  
 ; OPERATING SYSTEM: Apple Operating System 7.5.5  
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/022,255  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: USSN 08/620,694  
 ; FILING DATE: 21 MARCH 1996  
 ; APPLICATION NUMBER: USSN 08/538,765  
 ; FILING DATE: 7 AUGUST 1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: USSN 08/410,535  
 ; FILING DATE: 23 MARCH 1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia Anne  
 ; REGISTRATION NUMBER: 34,695  
 ; REFERENCE/DOCKET NUMBER: 2617-B  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206)587-0430  
 ; TELEFAX: (206)  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 864 amino acids  
 ; TYPE: amino acid

TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-022-255-2  
 Query Match 7.61, Score: 306; DB 3; Length: 864;  
 Best Local Similarity 22.51; Pred. No. 8.2e-23;  
 Matches: 189; Conservative: 128; Mismatches: 319; Indels: 203; Gaps: 43;

QY 40 QWRM-----KAAAPRL-----CVANEGVGPASNSGLYNITKYNQCTYLPVVK 86  
 Db 17 GWLLLLNLVLPAGRASPRLLDPAPVCAQEGLSRVKNSTCLDDSWHPKNTLTPSPKNI 76  
 QY 87 HVIADANITISYACHDQAVT-ILWS-PGALGIEFLKFRVILEELKSEGRQCOQ---141  
 Db 77 YI-----NLSVSTQHGELVPLVHEWTLOTDASILEGAELSVLQATNERLCVKFOP 131  
 QY 142 --LILADPKQLNSFKTKGSESQPLNKKFTDYFKVVPFSPSIKKNESYHFFETTRAC-199  
 Db 132 LSLMQLHKKWRFSF-----SHFYDQGGQYETVTHLHPKPIPODPPHKSIIIFVDC 185  
 QY 200 D---LILQDONLACKFWKPRMLNI-----SQH-----GSDMOY 230  
 Db 186 EDSKMKATTSVSSGSLMDP-NITVETLDTQHLRVDTFLANESTPYQVLESFSDSEHS 244  
 QY 231 SFD-----HAPNFGFEFFLVHVKLKE---GPFKRKTKCKEQTTETTSCLL 274  
 Db 245 CFDVVKQIFAPROEEFHQANVTFTLSKFHCCHHVQVQFP--FSSCLND-----CLR 296  
 QY 275 QNVSPGDIYIELVDNTTKVMHVALKPV--HSP-WA-GPIRAVAITVPLVVISAFATL 330  
 Db 297 HAVTVPCPVI-----SNTT-----VPRPVADYIPLWVYGLITLAI-----LLGSVTL 341  
 QY 331 FTVCKRKOENIYSHLDESESTYTAALPRERLPRKPVFLCYSSKQGNHNVQOC 390  
 Db 342 IICHTWRLSGADQEKGDSDSKINGILPVADITPPPLPR-KWIVISA-DHPLYVEVLK 399  
 QY 391 PAYFLQFCCEVALDLMEDFSLCREGQREVIQK-----IHESQFIIVVCSKGMKYFDK 446  
 Db 400 FAQLITACGTEVALDLEEQVISEVGYMTWYSROKQEMVESNKKIILCSRG-----TQ 454  
 QY 447 KNYKHGG-----GRSGKGEFLVAVSAIAEKLQAKQSSAALSKEIAVYFDY 496  
 Db 455 AKWAILGMAEPVQLRCDHMKPAGDLFTAAANNMILPDFKR-----PACFGTVVYCFSG 509  
 QY 497 SC-EGDVPGILDSTKYRLMDNLPOLCSHLHSRDHGLQEPQ--HTROGSRNYFYSKSG 553  
 Db 510 ICSEKDVDFLNTSRYPMDREEV--YFRIQDLEMFEPGRMHVRELGDNYLQSPSG 567  
 QY 554 RSLYVAICNMHQFIDBEPDFKQFVFPHP-----PPLR---YREPVLEKFDGLVNDVM 606  
 Db 568 ROLKAVLRFOEMOTOCDFWFERENCLADGDLPSLDEEVEFDPLPP--GGGIVKQOPL 626  
 QY 607 CKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQD-----GEAR 648  
 Db 627 VRELP--SDGCLVYDVCV-----SEESRMALDQPMQRELVAHTLQSNVLPAGQV 677  
 QY 649 PALDGSAAQLPILRTYKAGSPDMP--RDS-----GIYDSSV---PSSELSLPL-----692  
 Db 678 PA---AHVVEPLHLPDGSAAQLPMTEDSEACPLLVQVORNSILCLPVDSDDLPLCSTPM 734  
 QY 693 -----MEGLSTDOTETSLTESVSSSGLGEEPEPALPSKLLSSGCKADLCGRSYTDE 746  
 Db 735 MSPDHLOGDAREQLESMLSVLQOSSLGQPLESNPR-PEVYLE-----GCTPSEEE 784

## RESULT 11

US-09-022-696-2  
 ; Sequence 2, Application US/09022696  
 ; Patent No. 6072037  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yao, Zhengbin  
 ; APPLICANT: Spriggs, Melanie  
 ; APPLICANT: Fauslow, William

TITLE OF INVENTION: No. 6072037el. Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Power Macintosh

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,696

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 864 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-022-696-2

Query Match 7.6%; Score 306; DB 3; Length 864;

Best Local Similarity 22.5%; Pred. No. 8.2e-23;

Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

QY 40 GRM-----KAAARPL-----CVANEGVGFASRNSGLYNITFYDNCITTYLNVPVK 86  
DB 17 GWLLLLNLVAPGRASPRLLDPAPVCAQEGLSRVKNSCLDSDMTHPKNLTTPSPKNI 76  
QY 87 RVIAADONITISYACHDOVAT-ILWS-PCALGIEELKGFVILSELKSEGRCCOQ--- 141  
DB 77 YI-----NLVSSTQHGELVPVLRVWTLQTDASILLEGAEUSVLQWNTNERLCVKQF 131  
QY 142 --LILKDPKOLNSSFRTKSGESOPFLNMKFETYVWVPFSPKINSYHFFFTTRAC 199  
DB 132 LSLMLQHKRKRWF-----SHFVDPQCEYEVTVHLPKPIPDGDPNHSKIIFVPC. 185  
QY 200 D---LLQPNLACKPFWKPRNLNI-----SQH-----GSDMQV 230  
DB 186 EDSKMKWTSCVSSGSLNDP-NITVETLDTQHLRVDTLWNESTPYQVLESFSESHS 244  
QY 231 SFD-----HAPNFGFRFFYLHYKLHE--GPFRKTKCKEOTETTSCLL 274  
DB 245 CFVWVKOIFAPROEEFHORANTYTLTSKPFHMCCHHVQVQPF-FSSCLND-----CLR 296  
QY 275 QNVSFGYIIELVDDNTTKVMYALAPV--HSP-WA-GPIRAVAITVPLVVISAFATL 330  
DB 297 HAVTVPCPVL-----SNTT-----VPRPVADYIPLWYGLTILAI-----LLVGSVIL 341  
QY 331 FVWCKRQKENIYSHLDESSESSTYTAALPRRLAPRKFVLCYSSKDGQNHNVQOC 390  
DB 342 ICTMTWRLSGADQEKRGDSKINGILPVADLTTPPLPR-KWIVTSA-DHPLVVEVWLK 399

QY 391 PAYFLODFCCCEVALDIEDFSLCREGQREVIQK-----THESQFIIVVCSKGMFYVDK 446  
DB 400 FAQLFLITACGTEVALDLEEQYISEGVYMTWVSRQKQMVESKRIILCSRG-----TO 454  
QY 447 KNYKHGG-----GRSGKGELFLVAVSAIAEKLRQAKQSSAALSFIAYFYDY.496  
DB 455 AKWAILGHAEPVAVQLRCDHMKPAGDLFTAAMNMLPDKFR-----PACFGYVVCYFSG 509  
QY 497 SC-EGDVPGLDLSLTRYLMONLPOLCSHLASRDBGLOEPCO--HTRQGRNRNYSKSG 553  
DB 510 ICSERDVPDLNTISRYPLADRFEV--YFRIQDLEMFEPGRMHRVRELTGNYLQSGSG 567  
QY 554 RSLYVAICNMHQFIDEEPWFKEQVPPHP-----PPLR--YREPVLKEDSGLVNDVM 606  
DB 568 ROLKEAVLRFQEWOTQCRDWFERENCLADGQDLPSLDEEVEFEDPLPP-GGIVKQOPL 626  
QY 607 CKPGPESDFCLKVEAAVLTGATGADSDSHESQHGGLDQD-----GEAR 648  
DB 627 VRELPSDGLVVDVCV-----SEESRMKLDLPQAPQRELAHTLQSLVPAEQV 677  
QY 649 PALDGSAALOPLHTYKAGSPDMR--RDS-----GIYDSSV--PSSELSLPL----- 692  
DB 678 PA-----AHVVEPLHLPDGSAAALPMTEDSBACPLLCVQVNSILCLPVDSDDLPLCSTM 734  
QY 693 -----MEGLSTQDTETSSLTSEVSSSGLGEEPPALPSKLLSSGCKADLCRSYTD 746  
DB 735 MSPDHLQGDAREQESLMSLVQLQSLSGOPLESNPR-PEVVL-----GCTSEEE 784

RESULT 12

US-08-978-773-2

Sequence 2, Application US/08978773

Patent No. 6083906

GENERAL INFORMATION:

APPLICANT: Troutt, Anthony

TITLE OF INVENTION: Method of Regulating Nitric Oxide Production

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple PowerMacintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,773

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/052,525

FILING DATE: 27 NOVEMBER 1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2623-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 864 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-978-773-2

Query Match 7.6%; Score 306; DB 3; Length 864;



Best Local Similarity 22.5%; Pred. No. 8.2e-23;  
Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

QY 40 GWRM-----KAAARPRL-----CVANEGVGPASRNSGLNITFKYDNCITYLNIPYVK 86  
DB 17 GWLLLLLVNAPGRASPRLLDPAPVCAQEGLSCKRVKNSCLDSDSHHPKNTPTSPKNI 76  
QY 87 HVIADAQNTISQYACHDOVAVT-ILWS-PGALGIEFLKGRVILELSEKSGRQCOO--- 141  
DB 77 YI-----NLSVSTQHGELVPVLHVETLQTDASILEGAEISVLQNTNRLCVKQF 131  
QY 142 --LILKDPKQNSFKRTGMSQPLNMFETDYFKVVPSPKKNESNYHFFETTRAC 199  
DB 132 LSQLQHRKRWFSE-----SHFVDPQGEYEVTVHLPKPIPDGPNHKSIIIFVPC 185  
QY 200 D---LILQPNLACKPFWKPRNLNI-----SOH-----GSDMOV 230  
DB 186 ESKRMKMTSCVSGSLWDP-NITVETLQTLQHLRVDFTLWNESTPYQVLESFSDSENHS 244  
QY 231 SFD-----HAPNFGREFYLYHKLKHE---GPFKRTCKQEQTTETTSCLL 274  
DB 245 CFDVVKQIFAPROEERHQRANVTFTLSKFHMCCHHVQVQPF-FSSCLND-----CLR 296  
QY 275 QNVSGDVIIELVDDTNTTKVMHYALKPV--HSP-NA-GPIRAVAITVPLVVISAFATL 330  
DB 297 HAVTVPCPVI-----SNTT-----VPRVADYIPLWYGLITLIAL-----LLVGSVIVL 341  
QY 331 FTVMCKKQENIYSHLDESSSESTYTAALPRERPRKPRPVLCYSSKDGQHNHNVQC 390  
DB 342 IICMTWRLSGADQEKHGDDSKINGILPVADLTPLPPLRPR-KWIVIVSA-DHPLYVEVWLK 399  
QY 391 FAYFLQDFCGCEVALDLWEDFSLCREGQREWIQK-----IHESOFILVVCSSKGMKYFVDK 446  
DB 400 FAPFLITACGTEVALDLLEQVISEGVVMTVSRQKQEMVESNKIILCSRG-----TQ 454

QY 447 KNYKHGG-----GRGSGKGLFVAVSAIAEKLRQAKOSSSAALSKEIAYFDY 496  
DB 455 AKWAILGWAEPVOLRCDHWKPGADLFTAMNMLPDKR-----PACFTYVVCYFSG 509  
QY 497 SC-EGDVGILDTKTKLMDNLPOLCSHLHSDHGLQEPQO---HTRQSGRRNYFRSKSG 553  
DB 510 ICSESDVDFNLSRYPLMDREEV--YFRIODLEMEFPCRMHVRRLTGDNYLQSPSG 567  
QY 554 RSLYALCNMHOVIDEEDPFEKQFVFPHP-----PPLR---YREPVLKEDSGVLNDVM 606  
DB 568 RQKEAVLRFQWOTQCPDFENLCLADGQDLFSLDEEVEDPLPP-GGIVIVQQLP 626  
QY 607 CKPGPESDCLKVEAAVIGATGPADSOHESQHGGLDQD-----GEAR 648  
DB 627 VRELPSGCLVVDVY-----SSEESRMALQPOLPQRELVAHTLQSMVLPAEQV 677  
QY 649 PALDGSALOPILHTVKAQSPSOMP-RDS-----GIVDSSV---PSSELSLPL----- 692  
DB 678 PA---AHVVEPLHLPDGSAAQLPMTEDSEACPILGVORNSILCLPVDSDDLPLCSTPM 734  
QY 693 -----NEGSLTDQTTESLSTESYSSGLGEZEPALPSKLKLSGCKADLCGRSTYDE 746  
DB 735 MSPDHLQGDAREQLSMLSVLOQSLSGOPLESWPR-PEVLE-----GCTPSEEE 784

RESULT 13  
US-09-022-253-2  
Sequence 2, Application US/09022253  
Patent No. 6096305  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fauslow, William  
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street

CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,253  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694  
FILING DATE: 21-MARCH-1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-253-2

Query Match 7.6%; Score 306; DB 3; Length 864;

Best Local Similarity 22.5%; Pred. No. 8.2e-23;  
Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

QY 40 GWRM-----KAAARPRL-----CVANEGVGPASRNSGLNITFKYDNCITYLNIPYVK 86  
DB 17 GWLLLLLVNAPGRASPRLLDPAPVCAQEGLSCKRVKNSCLDSDSHHPKNTPTSPKNI 76  
QY 87 HVIADAQNTISQYACHDOVAVT-ILWS-PGALGIEFLKGRVILELSEKSGRQCOO--- 141  
DB 77 YI-----NLSVSTQHGELVPVLHVETLQTDASILEGAEISVLQNTNRLCVKQF 131  
QY 142 --LILKDPKQNSFKRTGMSQPLNMFETDYFKVVPSPKKNESNYHFFETTRAC 199  
DB 132 LSQLQHRKRWFSE-----SHFVDPQGEYEVTVHLPKPIPDGPNHKSIIIFVPC 185  
QY 200 D---LILQPNLACKPFWKPRNLNI-----SOH-----GSDMOV 230  
DB 186 ESKRMKMTSCVSGSLWDP-NITVETLQTLQHLRVDFTLWNESTPYQVLESFSDSENHS 244  
QY 231 SFD-----HAPNFGREFYLYHKLKHE---GPFKRTCKQEQTTETTSCLL 274  
DB 245 CFDVVKQIFAPROEERHQRANVTFTLSKFHMCCHHVQVQPF-FSSCLND-----CLR 296  
QY 275 QNVSGDVIIELVDDTNTTKVMHYALKPV--HSP-NA-GPIRAVAITVPLVVISAFATL 330  
DB 297 HAVTVPCPVI-----SNTT-----VPRVADYIPLWYGLITLIAL-----LLVGSVIVL 341  
QY 331 FTVMCKKQENIYSHLDESSSESTYTAALPRERPRKPRPVLCYSSKDGQHNHNVQC 390  
DB 342 IICMTWRLSGADQEKHGDDSKINGILPVADLTPLPPLRPR-KWIVIVSA-DHPLYVEVWLK 399  
QY 391 FAYFLQDFCGCEVALDLWEDFSLCREGQREWIQK-----IHESOFILVVCSSKGMKYFVDK 446  
DB 400 FAPFLITACGTEVALDLLEQVISEGVVMTVSRQKQEMVESNKIILCSRG-----TQ 454

QY 447 KNYKHGG-----GRSGKGELFLVAVSAIAEKLROAKQSSAALSXFIAYFDY 496  
 DB 455 AKWAILGWAEPVQLRCHWRKPADGLFTAAANNILPDKR-----PACFGYVVCYFSG 509  
 QY 497 SC-EDVPGILDSTKRYLNDNLQCLSHLSRDBGLQBPQ--HTRQSSRNRYFRSG 553  
 DB 510 ICSEKVDPLNITTSRYPLMDRFEV--YFRIQDLEMFEPGRHHVREITGDNYSQSPG 567  
 QY 554 RSLYVAICNHOPIDEPWFKEQFVPPHP-----PPLR--YREPVLKFDGSLVNDVM 606  
 DB 568 ROLKEAVLRFQEMOTQCPDWFERNICLADGQDPLSDEEVEFDPLPP--GGGIVKQOPL 626  
 QY 607 CKPGESDFCLVEAIVLGATGPADSOHESQHGGLDQ-----GEAR 648  
 DB 627 VRELPSGCLVVDVCV-----SEESRNKLDLPOLPQRELVAHTLQSWLPAEQV 677  
 QY 649 PALDGSAAALQPLHTVKAGSPDMP--RDS-----GIYDSSV--PSSELSLPL----- 692  
 DB 678 PA--AHVVEPLHLPDGSAAALQPLMTEDSEACPLLGVRNSILCLPVDSDOLPLCSTPM 734  
 QY 693 -----MEGLSTDQTTSSLTSESVSSSGIGEEPPALPSKLLSSGCKADLCRSYTD 746  
 DB 735 MSPDHLOQDAREQLSMLSVLQOQSLGQPLESWPR-PEVLE-----GCTPSEEE 784

## RESULT 14

US-09-022-260-2

Sequence 2, Application US/09022260

Patent No. 6100235

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESS: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,260

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 864 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-022-260-2

Query Match 7.69; Score 306; DB 3; Length 864;

Best Local Similarity 22.59; Pred No. 8.2e-23;

Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

QY 40 GWRM-----KAARPRL-----CVANEGVGPASRNSGLNITFKYDNCNTTYLNVPGR 86

DB 17 GWLLILNVLARSPRLDFFAPVCAQOGLSCRVKNSTCLDDSDWIHPKNTLSPSPKNI 76

QY 87 HVIADQNTISQACHQDAVT--ILMS--PCALGIBFLAGFVFLVLEELKSGRCQOQ--- 141

DB 77 YI-----NLSVSTQHGELVPLVHVEWTLQTDASILYLEGAELSVLQNLNRLCVRFQF 131

QY 142 --LILKDPQLNSKPKRTGMSQOPFLNKKFTETDFYKVVPPFPFSIKNESNYHFFTRAC 199

DB 132 LSMQHRKRWRFSE-----SHFVVDPGQYEVTVHHLKPIPDGDPNHHKSKIIFFPDC 185

QY 200 D-----LILQPDNLACKPFPKPRNLNI---SQH-----GSDMQV 230

DB 186 EDSKMKNTTSCYSSGSLMDP--NITVETLDQHLRVDTLANESTPVQVLESFSDSENHS 244

QY 231 SFD-----HAPHNFGFRFFLYHKLKHE---GPFKRYTCQEQTTTSCLL 274

DB 245 CFQVVKQIFAPROEFHORANVTFLSKFWCCHHVVQVQPF--FSSCLND-----CLR 296

QY 275 QNVSPGDIILVDDTNTTRVMHYALKPV--HSP--WA--GPIRAVAITVPLVVISAFATL 330

DB 297 HAVTVPCPI-----SNTT-----VPKPVADYPLWVYGLITLAI-----LLVGSVIL 341

QY 331 FTVWCRKQOENIYSHLDSESESTYTAALPRERLRPRKPKVPLCYSSKQCONHNVQOC 390

DB 342 IICMTWELSGAQEKGDGSKINGILPVADLTTPPLRPR--KVIYVISA--DEPLIVEVVLK 399

QY 391 FAYFLQDFGCEVALDLMEDFSLCREGORWVIOK-----IHESQFIYVVCSGMKMYFDK 446

DB 400 FAOFLITAGCTEVALDLLEQVISEVGMTVWSRQKQEMVESNSKIIILCSRG-----TQ 454

QY 447 KNYKHGG-----GRSGKGELFLVAVSAIAEKLROAKQSSAALSXFIAYFDY 496

DB 455 AKWAILGWAEPVQLRCHWRKPADGLFTAAANNILPDKR-----PACFGYVVCYFSG 509

QY 497 SC-EDVPGILDSTKRYLNDNLQCLSHLSRDBGLQBPQ--HTRQSSRNRYFRSG 553

DB 510 ICSEKVDPLNITTSRYPLMDRFEV--YFRIQDLEMFEPGRHHVREITGDNYSQSPG 567

QY 554 RSLYVAICNHOPIDEPWFKEQFVPPHP-----PPLR--YREPVLKFDGSLVNDVM 606

DB 568 ROLKEAVLRFQEMOTQCPDWFERNICLADGQDPLSDEEVEFDPLPP--GGGIVKQOPL 626

QY 607 CKPGESDFCLVEAIVLGATGPADSOHESQHGGLDQ-----GEAR 648

DB 627 VRELPSGCLVVDVCV-----SEESRNKLDLPOLPQRELVAHTLQSWLPAEQV 677

QY 649 PALDGSAAALQPLHTVKAGSPDMP--RDS-----GIYDSSV--PSSELSLPL----- 692

DB 678 PA--AHVVEPLHLPDGSAAALQPLMTEDSEACPLLGVRNSILCLPVDSDOLPLCSTPM 734

QY 693 -----MEGLSTDQTTSSLTSESVSSSGIGEEPPALPSKLLSSGCKADLCRSYTD 746

DB 735 MSPDHLOQDAREQLSMLSVLQOQSLGQPLESWPR-PEVLE-----GCTPSEEE 784

## RESULT 15

US-09-022-259-2

Sequence 2, Application US/09022259

Patent No. 6191104

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE-ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING-SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,259  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/410,535  
FILING DATE: 23-MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 864 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-259-2

Query Match 7.64; Score 306; DB 4; Length 864;  
Best Local Similarity 22.54; Pred. No. 8.2e-23;  
Matches 189; Conservative 128; Mismatches 319; Indels 203; Gaps 43;

QY 40 GNRM-----KAAARPR-----CVANEGVPASRNSGLNTEKYDNCITLYNPVK 86  
DB 17 GWLLLLNVLAGRASPLLDFAFVCAQEGLSCKVKNSTCLDSDSWHPKNTLTPSPKNI 76  
QY 87 HVIADQNTISQYACHDQAVT-ILWS-PGALGIEFLKGRVILEELKSEGRQCOO---141  
DB 77 YI-----NLVSSTGHGELVPLHVEVTLQTDASILYLEGAELSVLQNTNERLCVKFQF 131  
QY 142 --LILKDPKQLMSSPKTGMESQPLNMKFETDYFKVVPVPSIKNESYHPEFFRTRAC 199  
DB 132 LSHLQHRKRWRFSF-----SHEVDPOGEYEVVHHLPRPDGDPNHSKLIIFVDC 185  
QY 200 D---LLLPDNLACKPFWKPRNLAI-----SQH-----GSDMQV 230  
DB 186 EDSEKMTWTSVSSGSLMDP-NITVETLDTQHLRVDFTLWNESTPYQVLLSEFSSENHS 244  
QY 231 SFD-----HAPHNFGFRFFLYHLKHE---GPKRCKQBOETTETSCLL 274  
DB 245 CFDVVKQIPAPQEFHORANVTFLSKFWCCHHHVQVQFP-RSSCLND-----CLR 296  
QY 275 QNVSPGDYIIELVDTNTRKVIYALKPV--HSP-WA-GPIRAVAITVPLVWISAFATL 330  
DB 297 HAVTVPCPI-----SNT-----VPRVADYIPLWYGLITLAI---LLVGSVIL 341  
QY 331 FTWCKKQOENIYSHLDESSSESTYALPRRLRPRKPVFLCYSSKDGONHMYVQC 390  
DB 342 IICMTWRLSGDOERKGDSDKINGILLPVADLTPPLRPR-KWIVYSA-DHPLYVEVLK 399  
QY 391 FAYFLQDGCQVADLWEDFSLCQREWIQK-----IHESQFIIVVCSKGMKYFDK 446

DB 400 FAQLITACGTEVALDLLEEQVISEGVNTWVSROKQENVESNKIILCSRG-----TO 454  
QY 447 KNYKHKGG-----GRSGKGELELVAVSAIAEKLRQAKQSSSAALSXFIAYFDY 496  
DB 455 AKKAILGMAEPAPVQLRCDHMKPAGDLFTAAMNMLPDFER-----PACFGYVVCYFSG 509  
QY 497 SC-EGDVPGLDILSTKYRLMDNLPOLCSHLHSRDHGLQESG--HTROGSRNYSKSG 553  
DB 510 ICSDRVDPLFNITSRYPLMDRFEV--YFIQLEMFEGFRMHRVREUTGNYLQSFSG 567  
QY 534 RSLYVAICNMHQFIDBEPWFQKFPVPHF--PPLR--YREPVLKFDGLVNDVM 606  
DB 568 RQLKEAVLRFQEWOTQCPQWFERENLCLADGQDLPSLDEEVFEDPLPP-GGGIVKQOPL 626  
QY 607 CKPGPESDFCLKYEMAATLGNATGPADSOHESOHGGLDQ-----GEAR 648  
DB 627 VRELP-SDGCLVVDVY-----SEESRMALDPOLHPQRELVHATLQSNVLPABQV 677  
QY 649 PALDGSAAALQPLHHTVKAGSPDMP--RDS-----GIYDSV--PSSLSLPL-----692  
DB 678 PA---AHVVEPLHLPDGSAGAAQLPMTEDSEACPLLAGVQANSILCLPVDSDDLPLCSTPM 734  
QY 693 -----MEGLSTDQOTETSSLTESVSSSGIGBEEPPALPSPKLLSSGCKADLCGRSYTDE 746  
DB 735 MSPDHLQGDAREQLESIMLSVLQOSLSGQPLESNPR-PEVVLK-----GCTPSESE 784

Search completed: May 6, 2003, 13:46:17  
Job time : 34 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

# OM protein - protein search, using sv model

Run on: May 6, 2003, 13:44:51, Search time 24 Seconds  
(without alignments)  
2707.245 Million cell updates/sec

Title: US-09-912-157-2

Perfect score: 4013

Sequence: 1 MAPWLQCSVFTVNAACLG.....CTADLCGRSYTDEHAYAPL 753

Scoring table: BLOSUM62

Gapop: 10.0, Gapext 0.5

Searched: 328255 seqs, 8628685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database:

- Published Applications AA:\*
- 1: /cgn2.6/ptodata/1/pubpaa/US08\_NEW\_PUB.pap.\*
  - 2: /cgn2.6/ptodata/1/pubpaa/PC2\_NEW\_PUB.pap.\*
  - 3: /cgn2.6/ptodata/1/pubpaa/US06\_NEW\_PUB.pap.\*
  - 4: /cgn2.6/ptodata/1/pubpaa/US06\_PUBCOMB.pap.\*
  - 5: /cgn2.6/ptodata/1/pubpaa/US07\_NEW\_PUB.pap.\*
  - 6: /cgn2.6/ptodata/1/pubpaa/US07\_PUBCOMB.pap.\*
  - 7: /cgn2.6/ptodata/1/pubpaa/PC2US\_PUBCOMB.pap.\*
  - 8: /cgn2.6/ptodata/1/pubpaa/US08\_PUBCOMB.pap.\*
  - 9: /cgn2.6/ptodata/1/pubpaa/US09\_NEW\_PUB.pap.\*
  - 10: /cgn2.6/ptodata/1/pubpaa/US09\_PUBCOMB.pap.\*
  - 11: /cgn2.6/ptodata/1/pubpaa/US10\_NEW\_PUB.pap.\*
  - 12: /cgn2.6/ptodata/1/pubpaa/US10\_PUBCOMB.pap.\*
  - 13: /cgn2.6/ptodata/1/pubpaa/US60\_NEW\_PUB.pap.\*
  - 14: /cgn2.6/ptodata/1/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4013	100.0	753	9	US-09-912-157-2
2	4003	99.8	753	9	US-09-912-157-5
3	3925	97.8	739	9	US-09-912-157-8
4	3901	97.2	738	10	US-09-809-567-2
5	3703	92.3	728	9	US-09-874-503-18
6	3703	92.3	728	9	US-10-000-157-18
7	3703	92.3	728	9	US-09-816-744-18
8	3703	92.3	728	9	US-09-747-259-18
9	3703	92.3	728	9	US-09-908-827-18
10	3387	84.4	739	9	US-09-912-157-12
11	312	7.8	810	10	US-09-809-567-3
12	312	7.8	866	10	US-09-778-971-9
13	312	7.8	866	12	US-10-033-522-1
14	135.5	3.4	502	9	US-09-874-503-12
15	135.5	3.4	502	9	US-10-000-157-12
16	135.5	3.4	502	9	US-10-063-547-158
17	135.5	3.4	502	9	US-09-816-744-12
18	135.5	3.4	502	9	US-09-747-259-12
19	135.5	3.4	502	9	US-10-174-590-400

20	135.5	3.4	502	9	US-10-176-758-400	Sequence 400, App
21	135.5	3.4	502	9	US-10-063-616-158	Sequence 158, App
22	135.5	3.4	502	9	US-10-175-737-400	Sequence 400, App
23	135.5	3.4	502	9	US-10-063-502-158	Sequence 158, App
24	135.5	3.4	502	9	US-10-173-706-400	Sequence 400, App
25	135.5	3.4	502	9	US-10-175-738-400	Sequence 400, App
26	135.5	3.4	502	9	US-10-175-752-400	Sequence 400, App
27	135.5	3.4	502	9	US-10-176-482-400	Sequence 400, App
28	135.5	3.4	502	9	US-10-176-757-400	Sequence 400, App
29	135.5	3.4	502	9	US-10-176-913-400	Sequence 400, App
30	135.5	3.4	502	9	US-10-180-552-400	Sequence 400, App
31	135.5	3.4	502	9	US-10-180-557-400	Sequence 400, App
32	135.5	3.4	502	9	US-10-173-700-400	Sequence 400, App
33	135.5	3.4	502	9	US-10-174-572-400	Sequence 400, App
34	135.5	3.4	502	9	US-10-174-579-400	Sequence 400, App
35	135.5	3.4	502	9	US-10-174-582-400	Sequence 400, App
36	135.5	3.4	502	9	US-10-174-588-400	Sequence 400, App
37	135.5	3.4	502	9	US-10-175-739-400	Sequence 400, App
38	135.5	3.4	502	9	US-10-175-740-400	Sequence 400, App
39	135.5	3.4	502	9	US-10-176-488-400	Sequence 400, App
40	135.5	3.4	502	9	US-10-176-492-400	Sequence 400, App
41	135.5	3.4	502	9	US-10-176-747-400	Sequence 400, App
42	135.5	3.4	502	9	US-10-176-750-400	Sequence 400, App
43	135.5	3.4	502	9	US-10-176-985-400	Sequence 400, App
44	135.5	3.4	502	9	US-10-176-987-400	Sequence 400, App
45	135.5	3.4	502	9	US-10-176-987-400	Sequence 400, App

## ALIGNMENTS

### RESULT 1

US-09-912-157-2  
; Sequence 2, Application US/09912157  
; Patent No. US20020165348A1  
; GENERAL INFORMATION:  
; APPLICANT: Priesnell, Scott R.  
; APPLICANT: Kuestner, Rolf E.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: Human Cytokine Receptor  
; FILE REFERENCE: 00-49  
; CURRENT APPLICATION NUMBER: US/09/912.157  
; CURRENT FILING DATE: 2001-07-23  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 753  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-157-2

Query Match 100.0%; Score 4013; DB 9; Length 753;  
Best Local Similarity: 100.0%; Pred. No. 0;  
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	MAPWLQCSVFTVNAACLG	SO	LA	AGSGRAGDTCGRMKAARPRLCVANEVGP	60
DB	1	MAPWLQCSVFTVNAACLG	SO	LA	AGSGRAGDTCGRMKAARPRLCVANEVGP	60
OY	61	ASRNSGLNITFKYDNCITTYLNPVGRHVIAQAQNTISQYACHDQVAVTILMSPGALGIE	120			
DB	61	ASRNSGLNITFKYDNCITTYLNPVGRHVIAQAQNTISQYACHDQVAVTILMSPGALGIE	120			
OY	121	FLKGRVILEELKSGRCCQLIKDPQLNSFKRTGMSQPLNKKFTETDFYKVVVVF	180			
DB	121	FLKGRVILEELKSGRCCQLIKDPQLNSFKRTGMSQPLNKKFTETDFYKVVVVF	180			
OY	181	PSIKNSNYHPFFTRACDILLQPDNLACKPFWKPNLNISQSGDMQVSDHAPHNFG	240			
DB	181	PSIKNSNYHPFFTRACDILLQPDNLACKPFWKPNLNISQSGDMQVSDHAPHNFG	240			
OY	241	FRFYLHYKLKGGPKRTCKQEQTTTSCLLQNSPGDYITIELVDVDTNTRKVVHYA	300			

Db 241 PRFFYLHYKHEGPFKRTCKQOTTTETSCLLQNVSPDYIELVDDTNTTRKVMHYA 300  
QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSSTYTA 360  
Db 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSSTYTA 360  
QY 361 LPRERLRPRKPVFLCYSSKQDNHNNVQCFATFLQDFCGCEVALDLWEDFSLCREGORE 420  
Db 361 LPRERLRPRKPVFLCYSSKQDNHNNVQCFATFLQDFCGCEVALDLWEDFSLCREGORE 420  
QY 421 WVIQKHESQFIIVVCSKGMKIFVCKKNTYKHGGGSGKGELEFLVAVSAIAEKLRAQK 480  
Db 421 WVIQKHESQFIIVVCSKGMKIFVCKKNTYKHGGGSGKGELEFLVAVSAIAEKLRAQK 480  
QY 481 SSSAALSXFIAYFDYSCGDDVPGIILDSTKYRLMDNLPQLCSHLHSDHGLQEPQOHTR 540  
Db 481 SSSAALSXFIAYFDYSCGDDVPGIILDSTKYRLMDNLPQLCSHLHSDHGLQEPQOHTR 540  
QY 541 QGSRNRYFRSKGSLYVAICNMHOFIDEEPDMFEKQFVFPFHPPLRYREPVLEKFDGSL 600  
Db 541 QGSRNRYFRSKGSLYVAICNMHOFIDEEPDMFEKQFVFPFHPPLRYREPVLEKFDGSL 600  
QY 601 VLNDVCKPGPESDFCLVAAVLGATGADSPADSHQSGHGLQDGEARPAALDGSAAALQPL 660  
Db 601 VLNDVCKPGPESDFCLVAAVLGATGADSPADSHQSGHGLQDGEARPAALDGSAAALQPL 660  
QY 661 LHTVAGSPDMRDSGIYDSSVPSSLSPLMEGLSTDTQETSSLSVESSSSGLGEE 720  
Db 661 LHTVAGSPDMRDSGIYDSSVPSSLSPLMEGLSTDTQETSSLSVESSSSGLGEE 720  
QY 721 PPALPSKLLSSGCKADLCGRSYTDELHVAAPL 753  
Db 721 PPALPSKLLSSGCKADLCGRSYTDELHVAAPL 753

## RESULT 2

US-09-912-157-5

; Sequence 5, Application US/09912157

; Patent No. US20020165348A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/09/912,157

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 753

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-912-157-5

Query Match 99.8%; Score 4003; DB 9; Length 753;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 751; Conservative 0; Mismatches 2; Indels 0; Caps 0;

QY 1 MAPWLQCSVFTTVNACLSQLAAGSGRARGADTCGWRKMAAARPRCLVANEGVGP 60

Db 1 MAPWLQCSVFTTVNACLSQLAAGSGRARGADTCGWRKMAAARPRCLVANEGVGP 60

QY 61 ASRNSGLNITFKYDNCNTTYLNPVGRKVIADQNTISQYACHDOQVAVTILWSPGALGIE 120

Db 61 ASRNSGLNITFKYDNCNTTYLNPVGRKVIADQNTISQYACHDOQVAVTILWSPGALGIE 120

QY 121 FLKGRFVILEELKSGRQCOOLILKDPKQNSFKTGESOFFLNKMFETDYFVKVVPF 180

Db 121 FLKGRFVILEELKSGRQCOOLILKDPKQNSFKTGESOFFLNKMFETDYFVKVVPF 180

QY 181 PSIKNESNYHFFPFRACDILLQDNLACKPFWKPRNLNISQSGDMQVYFOHAPHNG 240

Db 181 PSIKNESNYHFFPFRACDILLQDNLACKPFWKPRNLNISQSGDMQVYFOHAPHNG 240

Db 181 PSIKNESNYHFFPFRACDILLQDNLACKPFWKPRNLNISQSGDMQVYFOHAPHNG 240  
QY 241 PRFFYLHYKHEGPFKRTCKQOTTTETSCLLQNVSPDYIELVDDTNTTRKVMHYA 300  
Db 241 PRFFYLHYKHEGPFKRTCKQOTTTETSCLLQNVSPDYIELVDDTNTTRKVMHYA 300  
QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSSTYTA 360  
Db 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSSTYTA 360  
QY 361 LPRERLRPRKPVFLCYSSKQDNHNNVQCFATFLQDFCGCEVALDLWEDFSLCREGORE 420  
Db 361 LPRERLRPRKPVFLCYSSKQDNHNNVQCFATFLQDFCGCEVALDLWEDFSLCREGORE 420  
QY 421 WVIQKHESQFIIVVCSKGMKIFVCKKNTYKHGGGSGKGELEFLVAVSAIAEKLRAQK 480  
Db 421 WVIQKHESQFIIVVCSKGMKIFVCKKNTYKHGGGSGKGELEFLVAVSAIAEKLRAQK 480  
QY 481 SSSAALSXFIAYFDYSCGDDVPGIILDSTKYRLMDNLPQLCSHLHSDHGLQEPQOHTR 540  
Db 481 SSSAALSXFIAYFDYSCGDDVPGIILDSTKYRLMDNLPQLCSHLHSDHGLQEPQOHTR 540  
QY 541 QGSRNRYFRSKGSLYVAICNMHOFIDEEPDMFEKQFVFPFHPPLRYREPVLEKFDGSL 600  
Db 541 QGSRNRYFRSKGSLYVAICNMHOFIDEEPDMFEKQFVFPFHPPLRYREPVLEKFDGSL 600  
QY 601 VLNDVCKPGPESDFCLVAAVLGATGADSPADSHQSGHGLQDGEARPAALDGSAAALQPL 660  
Db 601 VLNDVCKPGPESDFCLVAAVLGATGADSPADSHQSGHGLQDGEARPAALDGSAAALQPL 660  
QY 661 LHTVAGSPDMRDSGIYDSSVPSSLSPLMEGLSTDTQETSSLSVESSSSGLGEE 720  
Db 661 LHTVAGSPDMRDSGIYDSSVPSSLSPLMEGLSTDTQETSSLSVESSSSGLGEE 720  
QY 721 PPALPSKLLSSGCKADLCGRSYTDELHVAAPL 753  
Db 721 PPALPSKLLSSGCKADLCGRSYTDELHVAAPL 753

## RESULT 3

US-09-912-157-8

; Sequence 8, Application US/09912157

; Patent No. US20020165348A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/09/912,157

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 739

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-912-157-8

Query Match 97.8%; Score 3925; DB 9; Length 739;

Best Local Similarity 98.1%; Pred. No. 0;

Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MAPWLQCSVFTTVNACLSQLAAGSGRARGADTCGWRKMAAARPRCLVANEGVGP 60

Db 1 MAPWLQCSVFTTVNACLSQLAAGSGRARGADTCGWRKMAAARPRCLVANEGVGP 60

QY 61 ASRNSGLNITFKYDNCNTTYLNPVGRKVIADQNTISQYACHDOQVAVTILWSPGALGIE 120

Db 61 ASRNSGLNITFKYDNCNTTYLNPVGRKVIADQNTISQYACHDOQVAVTILWSPGALGIE 120

QY 121 FLKGRFVILEELKSGRQCOOLILKDPKQNSFKTGESOFFLNKMFETDYFVKVVPF 180

Db 121 FLKGRFVILEELKSGRQCOOLILKDPKQNSFKTGESOFFLNKMFETDYFVKVVPF 180

Db 107 FLKGRVILBELKSEGRQCOOLILKDPKOLNSFRKTMESQPFNNKFFDYFKVWPF 166  
QY 181 PSIKNESYHPPFFTRACDILLQPNLACKPFKPRNLNISQSGDMQVSPDHAPHNG 240  
Db 167 PSIKNESYHPPFFTRACDILLQPNLACKPFKPRNLNISQSGDMQVSPDHAPHNG 226  
QY 241 FRFFYLHLKHEGPFKTKCKOBTETTSCLLQNSPGDYIELVDDTNTTRKVMHYA 300  
Db 227 FRFFYLHLKHEGPFKTKCKOBTETTSCLLQNSPGDYIELVDDTNTTRKVMHYA 286  
QY 301 LKPVSPWAGIRAVAITVPLVISAFATLFTVMCKKQOENIYSHLDESSSESYTAA 360  
Db 287 LKPVSPWAGIRAVAITVPLVISAFATLFTVMCKKQOENIYSHLDESSSESYTAA 346  
QY 361 LPRERLRPRKPVFLCYSSKDGQNHNNVOCFAIFLDQFCGCEVALDLWEDFSLCREGORE 420  
Db 347 LPRERLRPRKPVFLCYSSKDGQNHNNVOCFAIFLDQFCGCEVALDLWEDFSLCREGORE 406  
QY 421 WYIQIHESQFIIVVCSKGMKYFVCKKNTKHKGGSGGSGKGEFLVAVSAIAEKLRAQK 480  
Db 407 WYIQIHESQFIIVVCSKGMKYFVCKKNTKHKGGSGGSGKGEFLVAVSAIAEKLRAQK 466  
QY 481 SSSAALSKFIAVFDYSCGDVPGILDSTKYRLMDNLPOLCSHLSDHGLQEPQOHR 540  
Db 467 SSSAALSKFIAVFDYSCGDVPGILDSTKYRLMDNLPOLCSHLSDHGLQEPQOHR 526  
QY 541 QGSRNTRFRSKGRSLVATCNHOFIDEEPDMFEKQFVPPHPPPLRYREPVLKFDL 600  
Db 527 QGSRNTRFRSKGRSLVATCNHOFIDEEPDMFEKQFVPPHPPPLRYREPVLKFDL 586  
QY 601 VLNDVCKPSPESDFCLKVEAAVLGATGPADSOHESQHGGLDQGEARPAALQPL 660  
Db 587 VLNDVCKPSPESDFCLKVEAAVLGATGPADSOHESQHGGLDQGEARPAALQPL 646  
QY 661 LHTVAGSPDMPRDSGIYDSSVPSSELSPLMEGLSTDTOTETSSLTSSVSSSGLGEE 720  
Db 647 LHTVAGSPDMPRDSGIYDSSVPSSELSPLMEGLSTDTOTETSSLTSSVSSSGLGEE 706  
QY 721 PPALPSKLLSSGCKADLCGRSYTDELHAPVL 753  
Db 707 PPALPSKLLSSGCKADLCGRSYTDELHAPVL 739

## RESULT 4

US-09-809-567-2  
; Sequence 2, Application US/09809567  
; Patent No. US20020045213A1  
; GENERAL INFORMATION:  
; APPLICANT: Jing, Shuguan  
; FILE REFERENCE: 01017/36916A  
; CURRENT APPLICATION NUMBER: US/09/809,567  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/724,460  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/189,816  
; PRIOR FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 738  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-567-2

Query Match 97.2%; Score 3901; DB 10; Length 738;

Best Local Similarity 97.6%; Pred. No. 0;

Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 1 MAPWQLQCSVFTVNAQLNGSQLVAAGSGRAGADTCGHRKAAARPLCVANEGVGP 60

Db 1 MAPWQLQCSVFTVNAQLNGSQLVAAGSGRAGADTCGHRKAAARPLCVANEGVGP 46

QY 61 ASRNSGLYNITFKYDNCITTLNPNVGRHVIAQAQNTISQYACHQDVAVTILSPGALGIE 120  
Db 47 ASRNSGLYNITFKYDNCITTLNPNVGRHVIAQAQNTISQYACHQDVAVTILSPGALGIE 106  
QY 121 FLKGRVILBELKSEGRQCOOLILKDPKOLNSFRKTMESQPFNNKFFDYFKVWVPF 180  
Db 107 FLKGRVILBELKSEGRQCOOLILKDPKOLNSFRKTMESQPFNNKFFDYFKVWVPF 166  
QY 181 PSIKNESYHPPFFTRACDILLQPNLACKPFKPRNLNISQSGDMQVSPDHAPHNG 240  
Db 167 PSIKNESYHPPFFTRACDILLQPNLACKPFKPRNLNISQSGDMQVSPDHAPHNG 226  
QY 241 FRFFYLHLKHEGPFKTKCKOBTETTSCLLQNSPGDYIELVDDTNTTRKVMHYA 300  
Db 227 FRFFYLHLKHEGPFKTKCKOBTETTSCLLQNSPGDYIELVDDTNTTRKVMHYA 286  
QY 301 LKPVSPWAGIRAVAITVPLVISAFATLFTVMCKKQOENIYSHLDESSSESYTAA 360  
Db 287 LKPVSPWAGIRAVAITVPLVISAFATLFTVMCKKQOENIYSHLDESSSESYTAA 346  
QY 361 LPRERLRPRKPVFLCYSSKDGQNHNNVOCFAIFLDQFCGCEVALDLWEDFSLCREGORE 420  
Db 347 LPRERLRPRKPVFLCYSSKDGQNHNNVOCFAIFLDQFCGCEVALDLWEDFSLCREGORE 406  
QY 421 WYIQIHESQFIIVVCSKGMKYFVCKKNTKHKGGSGGSGKGEFLVAVSAIAEKLRAQK 480  
Db 407 WYIQIHESQFIIVVCSKGMKYFVCKKNTKHKGGSGGSGKGEFLVAVSAIAEKLRAQK 466  
QY 481 SSSAALSKFIAVFDYSCGDVPGILDSTKYRLMDNLPOLCSHLSDHGLQEPQOHR 540  
Db 467 SSSAALSKFIAVFDYSCGDVPGILDSTKYRLMDNLPOLCSHLSDHGLQEPQOHR 526  
QY 541 QGSRNTRFRSKGRSLVATCNHOFIDEEPDMFEKQFVPPHPPPLRYREPVLKFDL 600  
Db 527 QGSRNTRFRSKGRSLVATCNHOFIDEEPDMFEKQFVPPHPPPLRYREPVLKFDL 586  
QY 601 VLNDVCKPSPESDFCLKVEAAVLGATGPADSOHESQHGGLDQGEARPAALQPL 660  
Db 587 VLNDVCKPSPESDFCLKVEAAVLGATGPADSOHESQHGGLDQGEARPAALQPL 646  
QY 661 LHTVAGSPDMPRDSGIYDSSVPSSELSPLMEGLSTDTOTETSSLTSSVSSSGLGEE 720  
Db 647 LHTVAGSPDMPRDSGIYDSSVPSSELSPLMEGLSTDTOTETSSLTSSVSSSGLGEE 706  
QY 721 PPALPSKLLSSGCKADLCGRSYTDELHAPVL 753  
Db 707 PPALPSKLLSSGCKADLCGRSYTDELHAPVL 739

## RESULT 5

US-09-874-503-18  
; Sequence 18, Application US/09874503  
; Patent No. US20020177188A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jian  
; APPLICANT: Filaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Hymowitz, Sarah G.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Starovasinik, Melissa A.  
; APPLICANT: VanLookenen, Menno  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Yansura, Daniel  
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

FILE REFERENCE: P1381R1CIP3(US)  
CURRENT APPLICATION NUMBER: US/09/874,503  
CURRENT FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/253,646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: US 60/244,072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: US 60/242,837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/175,481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: US 60/191,007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/213,807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 60/172,096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: US 60/138,387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: US 60/134,287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US 60/131,022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: US 60/130,232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: US 60/113,621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 60/085,579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: US 09/854,208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/854,280  
PRIOR FILING DATE: 2001-05-20  
PRIOR APPLICATION NUMBER: US 09/816,744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: US 09/747,259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US 09/644,848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: US 09/380,142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: US 09/380,138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: US 09/311,832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: US PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: US PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: US PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US PCT/US00/05601  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: US PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: US PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 18

LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-874-503-18  
Query Match 92.3%; Score 3703; DB 9; Length 728;  
Best Local Similarity 96.7%; Pred. No. 2.9e-307; Mismatches 8; Indels 14; Gaps 2;  
Matches 702; Conservative 2;  
QY 42 RKAAARPRLCVANE -GVGPASRNSGLNITFKYDNCNTTTLNPNVGVKHVITADAGNITISQY 100  
DB 3 RASASGVPALFVSGEQGVGPASRNSGLNITFKYDNCNTTTLNPNVGVKHVITADAGNITISQY 62  
QY 101 ACHDOQVAVTILMSPGALGIEFLKGFVILBELKSEGROCOOLILKDPKOLNSFFKRTGNE 160  
DB 63 ACHDOQVAVTILMSPGALGIEFLKGFVILBELKSEGROCOOLILKDPKOLNSFFKRTGNE 122  
QY 161 SPPFLNMKFETDYFVKVPPPSIKNESNYHPPFTRACDILLLOPONLACKPFWPRNLN 220  
DB 123 SPPFLNMKFETDYFVKVPPPSIKNESNYHPPFTRACDILLLOPONLACKPFWPRNLN 182  
QY 221 ISQ-----HGSDMOVSFDHAPHNFGFRFFLYHLKHEGPPKRRKCKOEQT 267  
DB 183 ISQHGSDMOVSFDHAPHNFGFRFFLYHLKHEGPPKRRKCKOEQT 242  
QY 268 ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327  
DB 243 EMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302  
QY 328 ATLFTVMCRKKQENIYSHLDEESSESSTYTAALPRERLRPRKRVFLCYSSKDGQNHMV 387  
DB 303 ATLFTVMCRKKQENIYSHLDEESSESSTYTAALPRERLRPRKRVFLCYSSKDGQNHMV 362  
QY 388 VOCFAFLODPGCEVALDLEDVSLCRGOREWVIOKIHESQFIIVVCSKGMKYPVDRK 447  
DB 363 VOCFAFLODPGCEVALDLEDVSLCRGOREWVIOKIHESQFIIVVCSKGMKYPVDRK 422  
QY 448 NYKHKGGRSGKGELFLVAVSAIAEKLRQAKQSSAALSFKFIATVFDYSCGDVPGILD 507  
DB 423 NYKHKGGRSGKGELFLVAVSAIAEKLRQAKQSSAALSFKFIATVFDYSCGDVPGILD 482  
QY 508 LSTKYLMDNLPOLCSHLHSRDRHGLQEPQCHTROGSRNNTFRSKSGRSLYVAICNNHQFI 567  
DB 483 LSTKYLMDNLPOLCSHLHSRDRHGLQEPQCHTROGSRNNTFRSKSGRSLYVAICNNHQFI 542  
QY 568 DEEDPWFEKQVPPHPPLRYREPVLKRPDGLVNDVCMKPGPESDFCLUKVEAAVILGAT 627  
DB 543 DEEDPWFEKQVPPHPPLRYREPVLKRPDGLVNDVCMKPGPESDFCLUKVEAAVILGAT 602  
QY 628 GPADSQHSQHGGLDQDGEARPALDGSAAALQPLLHTVKAGSPSDMPRDSGIDSSVPSSE 687  
DB 603 GPADSQHSQHGGLDQDGEARPALDGSAAALQPLLHTVKAGSPSDMPRDSGIDSSVPSSE 662  
QY 688 LSLPLMEGLSTDDTETSSLTSTSVSSSGGEEPPALPSKLLSSGCKADLGCRTYDEL 747  
DB 663 LSLPLMEGLSTDDTETSSLTSTSVSSSGGEEPPALPSKLLSSGCKADLGCRTYDEL 722  
QY 748 HAVAPL 753  
DB 723 HAVAPL 728

RESULT 6  
US-10-000-157-18  
Sequence 18, Application US/10000157  
Publication No. US20020182673A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Flivaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul L.  
APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillen, Kenneth J.  
APPLICANT: Hymowitz, Sarah  
APPLICANT: Tumas, Daniel  
APPLICANT: Starovasinik, Melissa  
APPLICANT: VanLookeren, Menno  
APPLICANT: Watanabe, Collin  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William  
APPLICANT: Yansura, Daniel  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1391R1C1P4(US)  
CURRENT APPLICATION NUMBER: US/10/000,157  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/130232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: 60/134287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/138387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/172096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/175481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: 60/191007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/213807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 60/242837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/244072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: 60/253646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 09/311832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/380138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/644848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 09/747259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/816744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 09/854208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/854280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/874503  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: 09/908827  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/929404  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 09/931836  
PRIOR FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/US99/31274

PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/US00/05601  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/21066  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
- NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 18  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-000-157-18

Query Match 92.3%; Score 3703; DB 9; Length 728;  
Best Local Similarity 96.7%; Pred. No. 2, 9e-307;

Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RKAAARPLCVANE-GVGPASRNSGLNITFKYDNCITLYLNPVKRVIAQDNITISQY 100  
DB 3 RASAGVPALFVSGEGVGVPASRNSGLNITFKYDNCITLYLNPVKRVIAQDNITISQY 62  
QY 101 ACHDOVAVTILWSPGALGIEFLAGFRVILEELKSEGRCCOOLILKDPKQNSFKRTGME 160  
DB 63 ACHDOVAVTILWSPGALGIEFLAGFRVILEELKSEGRCCOOLILKDPKQNSFKRTGME 122  
QY 161 SQPFLNMFETDYFKVYVPPSPKNSNYHPFFRTRACDLLLLQPDNLACKPFWKPNLN 220  
DB 123 SQPFLNMFETDYFKVYVPPSPKNSNYHPFFRTRACDLLLLQPDNLACKPFWKPNLN 182  
QY 221 ISO-----HGSDQVSVFCHAPNFGFFETLHYLKLKHEGPPFRKTKCKQSQT 267  
DB 183 ISOHGSDQVSVFCHAPNFGFFETLHYLKLKHEGPPFRKTKCKQSQT 242  
QY 268 ETTSCLLQNVSPGDYILIELVDNTTRKVMHVALKPVHSPWAGPIRAVAITVPLVISAF 327  
DB 243 EMTSCLLQNVSPGDYILIELVDNTTRKVMHVALKPVHSPWAGPIRAVAITVPLVISAF 302  
QY 328 ATLFTVMCKKQOENIYSHLDESSSTYTAALPRELRPRPKVFLCYSSKQSONHMY 387  
DB 303 ATLFTVMCKKQOENIYSHLDESSSTYTAALPRELRPRPKVFLCYSSKQSONHMY 362  
QY 388 VQCFATFLQDPCGCEVALDLWEDFSLCREGQREWIQKHESQFIIVVCSGKMKYFVDRK 447  
DB 363 VQCFATFLQDPCGCEVALDLWEDFSLCREGQREWIQKHESQFIIVVCSGKMKYFVDRK 422  
QY 448 NYKHKGGRSGSGKGLFLVAVSAIAEKLRQAKSSAALSKFIAVFDYCEGDVPGILD 507  
DB 423 NYKHKGGRSGSGKGLFLVAVSAIAEKLRQAKSSAALSKFIAVFDYCEGDVPGILD 482  
QY 508 LSTKYELNDNLPLCLSHLSHSDHCLQEPQGHTRQSGSRNYPKSGRSLVAICNMQFI 567



Db 483 LSTKYLMDNLPOLCSHLHSDHGLQEPQHTROGSRNTFRSKGSRSLYVAICNMHOFI 542  
QY 568 DEEDPWFKEQVFPFHPPLRYREPVLKFDGLVNDVCKPSPESDFCLKVEAAVLGAT 627  
Db 543 DEEDPWFKEQVFPFHPPLRYREPVLKFDGLVNDVCKPSPESDFCLKVEAAVLGAT 602  
QY 628 GPADSHQSHGGLDQDGEARPALDGSAAALQPLHTVYKAGSPDMPRDSGIYDSSVPSS 687  
Db 603 GPADSHQSHGGLDQDGEARPALDGSAAALQPLHTVYKAGSPDMPRDSGIYDSSVPSS 662  
QY 688 LSLPLMEGLSTQDTETSSLSYSSSSGSGEPEEPALPSKLLSSGCKADLCGRSYTDEL 747  
Db 663 LSLPLMEGLSTQDTETSSLSYSSSSGSGEPEEPALPSKLLSSGCKADLCGRSYTDEL 722  
QY 748 HAVAPL 753  
Db 723 HAVAPL 728

## RESULT 7

US-09-816-744-18

; Sequence 18, Application US/09816744

; Publication No. US20030003546A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Jian

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Li, Ranzhong

; APPLICANT: Hillan, Kenneth

; APPLICANT: Tamas, Daniel

; APPLICANT: VanLookeren, Menno

; APPLICANT: Vandlen, Richard

; APPLICANT: Watanabe, Colin

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William

; APPLICANT: Yansura, Daniel

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

; FILE REFERENCE: P1381R1C1P2(US)

; CURRENT APPLICATION NUMBER: US/09/816,744

; CURRENT FILING DATE: 2001-03-22

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 39

; SEQ ID NO 18

; LENGTH: 728

; TYPE: PRT

; ORGANISM: Homo Sapien.

US-09-816-744-18

Query Watch

Best Local Similarity 96.7%; Score 3703; DB 9; Length 728;

Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RMAAARPLCVANE-GVGPASRNSGLNITFKYDNCNTYTLNVPYKRVHVIADAQNTISQY 100  
Db 3 RASAGVPALFVSGEGVGPASRNSGLNITFKYDNCNTYTLNVPYKRVHVIADAQNTISQY 62  
QY 101 ACHDQVATVILWSPALGIEFLAGFRVILEELKSGRCQOOLILKOPKOLNSSFRKTGME 160  
Db 63 ACHDQVATVILWSPALGIEFLAGFRVILEELKSGRCQOOLILKOPKOLNSSFRKTGME 122  
QY 161 SQPLNAPETDYFVKVVPSPSILKNSNTHPFFRTRACDILLQPNLACKPFWKPRNLN 220  
Db 123 SQPLNAPETDYFVKVVPSPSILKNSNTHPFFRTRACDILLQPNLACKPFWKPRNLN 182  
QY 221 ISO-----HGSDMQVSDFAHNGSDMQVSDFAHNGFRFFYLLHKLKHEGFFRKTCKQEQTT 267  
Db 183 ISOHGSDMQVSDFAHNGSDMQVSDFAHNGFRFFYLLHKLKHEGFFRKTCKQEQTT 242

## RESULT 8

US-09-747-259-18

; Sequence 18, Application US/09747259

; Publication No. US20030008815A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Chen, Jian

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Li, Ranzhong

; APPLICANT: Hillan, Kenneth

; APPLICANT: Tamas, Daniel

; APPLICANT: VanLookeren, Menno

; APPLICANT: Vandlen, Richard

; APPLICANT: Watanabe, Colin

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William

; APPLICANT: Yansura, Daniel

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

; FILE REFERENCE: P1381R1C1P1(US)

; CURRENT APPLICATION NUMBER: US/09/747,259

; CURRENT FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: US 09/311,832

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: US 60/172,096

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: PCT/US99/31274

; PRIOR FILING DATE: 1999-12-30

; PRIOR APPLICATION NUMBER: US 60/175,481

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: PCT/US00/04341

; PRIOR FILING DATE: 2000-02-16

QY 268 ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPHAGPVRVAIVTVPVLSAF 327  
Db 243 EMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPHAGPVRVAIVTVPVLSAF 302  
QY 328 ATLEFVNCRKQOENIYSHLDESESESTYTAALPRERLRPRKVPFLCYSSKQDGNHNV 387  
Db 303 ATLEFVNCRKQOENIYSHLDESESESTYTAALPRERLRPRKVPFLCYSSKQDGNHNV 362  
QY 388 VQCFAYFLQDFCCEVALDLMEDFSLCREGQREWVIOKIHESOFIIVVCSKGMKIFYDKK 447  
Db 363 VQCFAYFLQDFCCEVALDLMEDFSLCREGQREWVIOKIHESOFIIVVCSKGMKIFYDKK 422  
QY 448 NYKHGGGSGRGELFLVAVSAIAEKLRQAKQSSAALSFKFIAYFYDSCGDPVGLD 507  
Db 423 NYKHGGGSGRGELFLVAVSAIAEKLRQAKQSSAALSFKFIAYFYDSCGDPVGLD 482  
QY 508 LSTKYRLMDNLPOLCSHLHSDHGLQEPQHTROGSRNTFRSKGSRSLYVAICNMHOFI 567  
Db 483 LSTKYRLMDNLPOLCSHLHSDHGLQEPQHTROGSRNTFRSKGSRSLYVAICNMHOFI 542  
QY 568 DEEDPWFKEQVFPFHPPLRYREPVLKFDGLVNDVCKPSPESDFCLKVEAAVLGAT 627  
Db 543 DEEDPWFKEQVFPFHPPLRYREPVLKFDGLVNDVCKPSPESDFCLKVEAAVLGAT 602  
QY 628 GPADSHQSHGGLDQDGEARPALDGSAAALQPLHTVYKAGSPDMPRDSGIYDSSVPSS 687  
Db 603 GPADSHQSHGGLDQDGEARPALDGSAAALQPLHTVYKAGSPDMPRDSGIYDSSVPSS 662  
QY 688 LSLPLMEGLSTQDTETSSLSYSSSSGSGEPEEPALPSKLLSSGCKADLCGRSYTDEL 747  
Db 663 LSLPLMEGLSTQDTETSSLSYSSSSGSGEPEEPALPSKLLSSGCKADLCGRSYTDEL 722  
QY 748 HAVAPL 753  
Db 723 HAVAPL 728

## RESULT 8

US-09-747-259-18

; Sequence 18, Application US/09747259

; Publication No. US20030008815A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Chen, Jian

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Li, Ranzhong

; APPLICANT: Hillan, Kenneth

; APPLICANT: Tamas, Daniel

; APPLICANT: VanLookeren, Menno

; APPLICANT: Vandlen, Richard

; APPLICANT: Watanabe, Colin

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William

; APPLICANT: Yansura, Daniel

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

; FILE REFERENCE: P1381R1C1P1(US)

; CURRENT APPLICATION NUMBER: US/09/747,259

; CURRENT FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: US 09/311,832

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: US 60/172,096

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: PCT/US99/31274

; PRIOR FILING DATE: 1999-12-30

; PRIOR APPLICATION NUMBER: US 60/175,481

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: PCT/US00/04341

; PRIOR FILING DATE: 2000-02-16

PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 60/191,007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: US 60/213,087  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 09/644,848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/242,837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: US 60/253,646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 18  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-747-259-18

Query Match 92.3%; Score 3703; DB 9; Length 728;  
Best Local Similarity 96.7%; Pred. No. 2.9e-307;  
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RKMAARPRICVAHE-CVGPASRNSGLNITFKYDNCNTYLPVGVHVTADAQNTISQY 100  
DB 3 RASAGVPALFVGEQVGPASRNSGLNITFKYDNCNTYLPVGVHVTADAQNTISQY 62  
QY 101 ACHDOAVVITLWSPALGIEFLKGFVILEELKSEGRQCOOLILKDPKQLNSFKRTGME 160  
DB 63 ACHDOAVVITLWSPALGIEFLKGFVILEELKSEGRQCOOLILKDPKQLNSFKRTGME 122  
QY 161 SPTLWKFEDYFVKVPPSPKSNESNYHFFETRACDLLOPDLNACKPFWKPRNLN 220  
DB 123 SPTLWKFEDYFVKVPPSPKSNESNYHFFETRACDLLOPDLNACKPFWKPRNLN 182  
QY 221 ISQ-----HGSDMQVSFDHAPHNFGRFFVLYHKLKHEGPKRKTCKQEQTT 267  
DB 183 ISQHGSDMQVSFDHAPHNFGRFFVLYHKLKHEGPKRKTCKQEQTT 242  
QY 268 ETTSCLLQNVSPGDIIEELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327  
DB 243 EMTSCLLQNVSPGDIIEELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302  
QY 328 ATLPTVMCKKQENIYSHLDESSSTYTAALPRELRPRKRVFLCYSSKDGQNHNV 387  
DB 303 ATLPTVMCKKQENIYSHLDESSSTYTAALPRELRPRKRVFLCYSSKDGQNHNV 362  
QY 388 VCFAYFLQDPCGCEVALDWEFSLCRGQREWIQIHESQFIIVVCSKGMKFFVDKK 447  
DB 363 VCFAYFLQDPCGCEVALDWEFSLCRGQREWIQIHESQFIIVVCSKGMKFFVDKK 422  
QY 448 NTKHKGGRSGKGFELVAVASIAEKLKRAQSSAALSXFIAVFDYSCGDVPGILD 507  
DB 423 NTKHKGGRSGKGFELVAVASIAEKLKRAQSSAALSXFIAVFDYSCGDVPGILD 482  
QY 508 LSTYRLMDNLPLCSEHLSDHGLQEPQHTROGSRNRTFRSKGRSLYVAICNHHQFI 567  
DB 483 LSTYRLMDNLPLCSEHLSDHGLQEPQHTROGSRNRTFRSKGRSLYVAICNHHQFI 542  
QY 568 DEEDPWFKEQVFPFPPPLRYREPVLKFDGSLVNDVMCKPGPESDFCLKVEAAVLGAT 627  
DB 543 DEEDPWFKEQVFPFPPPLRYREPVLKFDGSLVNDVMCKPGPESDFCLKVEAAVLGAT 602

QY 628 GPADQSHQSGGLDQDGEARFALDGSAAQLLHTVTKAGSPDMPROSGIYDSSVPSSE 687  
DB 603 GPADQSHQSGGLDQDGEARFALDGSAAQLLHTVTKAGSPDMPROSGIYDSSVPSSE 662  
QY 688 LSLPLMEGLSTDTQETSSLTSSVSSSGGLGEEPPALPSKLLSSGCKADLZGCRSYTDEL 747  
DB 663 LSLPLMEGLSTDTQETSSLTSSVSSSGGLGEEPPALPSKLLSSGCKADLZGCRSYTDEL 722  
QY 748 HAVAPL 753  
DB 723 HAVAPL 728

## RESULT 9

US-09-908-827-18.

Sequence 18, Application US/09908827

Publication No. US20030054442A1

GENERAL INFORMATION:

APPLICANT: Chen, Jian

APPLICANT: Fillvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

APPLICANT: Li, Hanzhong

APPLICANT: Hillan, Kenneth

APPLICANT: Tumas, Daniel

APPLICANT: VanLookeren, Menno

APPLICANT: Vandlen, Richard

APPLICANT: Watanabe, Colin

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William

APPLICANT: Yansura, Daniel

TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

FILE REFERENCE: P1301R1C1P1C1(US)

CURRENT APPLICATION NUMBER: US/09/908,827

CURRENT FILING DATE: 2001-07-18

PRIOR APPLICATION NUMBER: 60/085,579

PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/113,621

PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: 60/130,232

PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: 60/131,022

PRIOR FILING DATE: 1999-04-26

PRIOR APPLICATION NUMBER: 60/134,287

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 60/138,387

PRIOR FILING DATE: 1999-06-09

PRIOR APPLICATION NUMBER: 60/172,096

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/175,481

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: 60/191,007

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/213,807

PRIOR FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: 60/242,837

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: 60/244,072

PRIOR FILING DATE: 2000-10-26

PRIOR APPLICATION NUMBER: 09/311,832

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 09/380,138

PRIOR FILING DATE: 1999-08-25

PRIOR APPLICATION NUMBER: 09/380,142

PRIOR FILING DATE: 1999-08-25

PRIOR APPLICATION NUMBER: 09/644,848

PRIOR FILING DATE: 2000-08-22

PRIOR APPLICATION NUMBER: 09/747,259

PRIOR FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: 09/816,744



QY 420 EMTOKIHESQFIIVVCSGKMYFDKKNYKHGKGGSGKGEFLFVAVSAEKLROAK 479  
DB 407 EMTOKIHESQFIIVVCSGKMYFDKKNYKHGKGGSGKGEFLFVAVSAEKLROAK 466  
QY 480 QSSAALUSFTIAYFDYCEGDPGIDLSKYRLMDNIPOLCSHLRDRHGLQEP-GQH 538  
DB 467 QSSAALUSFTIAYFDYCEGDPGIDLSKYRLMDNIPOLCSHLRDRHGLQEP-GQH 523  
QY 539 TROSRNRYFRSGRSGLYVAICNNHOFIDEEPDMFEKQFVPPHPPPLRYREPVLKRFDS 598  
DB 534 PGHSSRNRYFRSGRSGLYVAICNNHOFIDEEPDMFEKQFVPPHPPPLRYREPVLKRFDS 593  
QY 599 GLVINDVMCKPGPESDFCLKVEAVALGATGPADSOH--RQHGGLDQGEARPALDGSAA 656  
DB 584 GLVINDVMCKPGPESDFCLKVEAVALGATGPADSOH--RQHGGLDQGEARPALDGSAA 643  
QY 657 LQPLHTVTKAGSPDMPSDGIYDSSVPSSELSLPLMEGLSTQDETSTLSYSSSSSGL 716  
DB 644 LQPLHTVTKAGSPDMPSDGIYDSSVPSSELSLPLMEGLSTQDETSTLSYSSSSSGL 703  
QY 717 GEREPPALSKLLSSGCKADLGCSYTDHHAVALP 753  
DB 704 GEREPPALSKLLSSGCKADLGCSYTDHHAVALP 739

## RESULT 11

US-09-809-567-3  
; Sequence 3, Application US/09809567  
; Patent No. US200045213A1  
; GENERAL INFORMATION:  
; APPLICANT: Jinq, Shuqian  
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof  
; FILE REFERENCE: 01017/36916A  
; CURRENT APPLICATION NUMBER: US/09/809,567  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR FILING DATE: 09/724,460  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR FILING DATE: 60/189,816  
; PRIOR FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 810  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-567-3

Query Match 7.88; Score 312; DB 10; Length 810;  
Best Local Similarity 23.18; Pred. No. 8.2e-18;  
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;  
QY 69 NITFKYDNC--TTLNPNVGRKVIADAGNIT-----ISQVACHDQ-----VAVTILWS 113  
DB 49 NCTVKNSTCLDDSWTHP-----RNLTPSSPKDLQIQLFAHTQGGDLFPVAHIEMT 99  
QY 114 -PCALGIEFLKGFVILEELKSGROCOOLILKDPOLNSSFKRTGMSQPFNNKFEYD 172  
DB 100 LQTDASILYLEGAEISVLQNLNRLCVR--FEFLSKLHHRRWRFTFSHFV-VDPDQE 156  
QY 173 YFKVY--VFPFSIKNESNYHFFTRACDLQLQPDNLACK---PFMKPRNL-----219  
DB 157 YEYVHLKPKIPDGDPNHQSKNFLVPDCSHARKMKTTPCMSSGSLMDP-NITVETLEAH 215  
QY 220 -----NISQSGDMQVFOHAPNFGFRFFLYLHKHKGPFKRTCKQQTETT 270  
DB 216 QLRVSTLWNESTHQILLTSFPMENHSCFEHMH-HIPAPRPEFHGRSVNTLRLNK 274  
QY 271 SCILQNVSGDYIIELVDT---NTRKVMHYALKPVHSGMAGPIRAVAITVPLWLSAF 327  
DB 275 GCRHQVQIQPFSSCLNDCLRHSATVSCPEMDTPETPIDVWPLWVWYFVITGISLLVG 334  
QY 328 ATLFTVMCKKQOENIYHLDBESSESTYTAALPRERLRPR-----NVFLCYSSKQSQN 363

DB 335 SVILLIVCMTRLAGPGS---EKYSDDTKYDGLPADLIPPLPKPKVMIISA-DHPL 390  
QY 384 HNNVOCFAIFLQDPCGEVALDLMEDFSLCRGQREW---TQKHESQFIIVVCSGK 439  
DB 391 YDVLVLAQFLLTACCTEVALDLEBEQAISEAGVNTWYGRQKQEMVESNKIIVLCSRG 450  
QY 440 MYFYVDKKNYKHGKGG-----RSGKGEFLFVAVSAEKLROAKQSSAALSKFTA 491  
DB 451 TR-----AKWQALGARGPVRLRCHGCKPVQDLTAAMNMLPDKER-----PACFGTYV 501  
QY 492 VTF-DYCEGDPGIDLSKYRLMDNIPOLCSHLRDRHGLQEPGQHTROG--SRNRYF 548  
DB 502 CYFSEYSCDGDVDFLFGAARPYPLMDRFEV--YFRIOOLEMFQGRHVRHVGELSGDNYL 559  
QY 549 RSKSGRSGLYVAICNNHOFIDEEPDMFE-----KQFVPPHPPPLRYREPVLKRFDSGL 600  
DB 560 RSPGGRLRAALDRFDQVRCVDFECENLYSADDDQAPSLDEEV-FEPELLPP-GTGI 617  
QY 601 VLNDVMCKPGPESDFCLKVEAVALGATGPADSOH-----SQHGG 640  
DB 618 YKRAPLVRE-PGSQACLAIDPLVCEBGGAAVAKLEPHLQPRQCPAPQPLHTVLAAEEGA 676  
QY 641 LDDGGEARPALDGSAA--ALQ-----PLLHTVTKAGSPDMPSDGIYDSSVPSSELSLP 691  
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QY 692 LMEGLSTQDETSTLSYSSSSGSGEPEPPALSKLLSSGCKADLGCC 740  
DB 728 L-GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEOGLSCQAGGCG 768

## RESULT 12

US-09-778-971-9  
; Sequence 9, Application US/09778971  
; Patent No. US20020102639A1  
; GENERAL INFORMATION:  
; APPLICANT: Shaughnessy, John D.  
; TITLE OF INVENTION: EV127 Gene Sequence and Protein Encoded Thereby  
; FILE REFERENCE: D6138  
; CURRENT APPLICATION NUMBER: US/09/778,971  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR FILING DATE: US 60/180,374  
; NUMBER OF SEQ ID NOS: 9  
; SEQ ID NO 9  
; LENGTH: 866  
; TYPE: PRT  
; ORGANISM: Unknown  
; NAME/KEY: peptide  
; OTHER INFORMATION: IL-17 receptor protein  
US-09-778-971-9

Query Match 7.88; Score 312; DB 10; Length 866;  
Best Local Similarity 23.18; Pred. No. 9.1e-18;  
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;  
QY 69 NITFKYDNC--TTLNPNVGRKVIADAGNIT-----ISQVACHDQ-----VAVTILWS 113  
DB 49 NCTVKNSTCLDDSWTHP-----RNLTPSSPKDLQIQLFAHTQGGDLFPVAHIEMT 99  
QY 114 -PCALGIEFLKGFVILEELKSGROCOOLILKDPOLNSSFKRTGMSQPFNNKFEYD 172  
DB 100 LQTDASILYLEGAEISVLQNLNRLCVR--FEFLSKLHHRRWRFTFSHFV-VDPDQE 156  
QY 173 YFKVY--VFPFSIKNESNYHFFTRACDLQLQPDNLACK---PFMKPRNL-----219  
DB 157 YEYVHLKPKIPDGDPNHQSKNFLVPDCSHARKMKTTPCMSSGSLMDP-NITVETLEAH 215  
QY 220 -----NISQSGDMQVFOHAPNFGFRFFLYLHKHKGPFKRTCKQQTETT 270  
DB 216 QLRVSTLWNESTHQILLTSFPMENHSCFEHMH-HIPAPRPEFHGRSVNTLRLNK 274

QY 271 SCLQNVSPGDIYIELVDOT---MTTRVNHIALKPVHSPWAGPIRAVAITVPLVWISAF 327  
DB 275 GCRHOVOIQPFSSCLNDLHSAIVSCPEMDTPEIPDYMPVWVWTFITGISILLVG 334  
QY 328 ATLTVNCRKQOENIYSHLDESESTYTAALPRERLRPR---KVFICYSSKQOON 383  
DB 335 SVILLVCMWRLAGPGS---EKYSDDTKYDGLPAADLPPPKRKRWIIYISA-DHPL 390  
QY 384 HNVVOCFAYFLQDFCGCEVALDLWEDFSLCRGQREW---IQIHESOFIIVVCSKG 439  
DB 391 YVDVLFKFAQLTACGTVEALDLLEQAISEAGVMTWGRQKQENVSNSIIVLCSRG 450  
QY 440 KMYFVDKKNYKHGGG---RGSGKGEFLVAVSAIAEKLRQAKOSSAALSRIA 491  
DB 451 TR---AKWQALLGRGAPVRLRCDHKGKPGVGLFTAAANNMLPDKR---PACFGTIVV 501  
QY 492 VYF-DYSCGDVPGIIDLSTKTRMLNDLPQLCSHLHSDRGHGLQEPQHTROG---SRRNYF 548  
DB 502 CYFEVSCDGVDPDLFGAAPRYPLMDRFEV---YFRIQDLEMPQGRMHRVGLSGDNYL 559  
QY 549 RSKSGSLYVAICNMHQFIDEEPWFE-----KQVFPFHPPLRYREPVLKFDOSGL 600  
DB 560 RSPGRLRAALDRFRDMQVRCDFECENLYSADDQDAPSLDEEV-PEEPLLP-GTGI 617  
QY 601 VLNDVCKPSPESDFCLKVEAAVILGATGPADSQHE-----SQHGG 640  
DB 618 VKRAPLVRE-PSQACLAIDLPLVGEEGAIAVAKLEPHLQPRGQAPQPLHTLVLAABEGA 676  
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DB 677 LVAAVEPGLADGAARLALAGEACPLGSPGAG-----RNSVLF---LPVDPEDSP 727  
QY 692 LMESLTDQETSSLESYSSSSGLGEEPPALPSKLLSSGCKADLGC 740  
DB 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAGGC 768

## RESULT 13

US-10-033-522-1

; Sequence 1, Application US/10033522

; Patent No. US20020136724A1

; GENERAL INFORMATION:

; APPLICANT: MOHLER, Kendall M.

; TITLE OF INVENTION: Methods for Treating Rheumatoid Arthritis Using IL-17 Antagonists

; FILE REFERENCE: 2982-A

; CURRENT APPLICATION NUMBER: US/10/033,522

; PRIOR FILING DATE: 2001-10-18

; PRIOR APPLICATION NUMBER: US 60/241,230

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 866

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-033-522-1

Query Match 7.8%; Score 312; DB 12; Length 866;

Best Local Similarity 23.1%; Pred. No. 9,1e-18;

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DB 49 NCTVKNSTCLDSDWHP-----RNLTPSPKDLQIQLHPAHTQOQDLFPVAHIEMT 99

QY 114 -PGALGIEFLKGFVILEELKSGROCOQLIKDKPKOLNSFKRTQKESQPLNKKFTED. 172

DB 100 LQTDASILYLEGAFLSVLQNTNRLCYR--FEFLSKLRHHRRWRFTSFHV-VDPQGE 156

QY 173 FVRYV--VPPPSIKNESNHPFFRTRACDILLQPDNLACK---PTWKPRNL----- 219

DB 157 YEVTVHLPKRPIDGPDNQHOSKRNFLVPCDHARMKVTTPCKSSGSLWDP-NITVTELEAH 215

QY 220 -----NISQSGDMQVSDHAPNFQFRFFYLHYLKHGEPFKRKTCKQSOTTETT 270  
DB 216 QLRVSTLANESTHYOILLTSPHMHNSCFEHHM-HIPAPPEEFHORSNVTILRNK 274  
QY 271 SCLQNVSPGDIYIELVDOT---MTTRVNHIALKPVHSPWAGPIRAVAITVPLVWISAF 327  
DB 275 GCRHOVOIQPFSSCLNDLHSAIVSCPEMDTPEIPDYMPVWVWTFITGISILLVG 334  
QY 328 ATLTVNCRKQOENIYSHLDESESTYTAALPRERLRPR---KVFICYSSKQOON 383  
DB 335 SVILLVCMWRLAGPGS---EKYSDDTKYDGLPAADLPPPKRKRWIIYISA-DHPL 390  
QY 384 HNVVOCFAYFLQDFCGCEVALDLWEDFSLCRGQREW---IQIHESOFIIVVCSKG 439  
DB 391 YVDVLFKFAQLTACGTVEALDLLEQAISEAGVMTWGRQKQENVSNSIIVLCSRG 450  
QY 440 KMYFVDKKNYKHGGG---RGSGKGEFLVAVSAIAEKLRQAKOSSAALSRIA 491  
DB 451 TR---AKWQALLGRGAPVRLRCDHKGKPGVGLFTAAANNMLPDKR---PACFGTIVV 501  
QY 492 VYF-DYSCGDVPGIIDLSTKTRMLNDLPQLCSHLHSDRGHGLQEPQHTROG---SRRNYF 548  
DB 502 CYFEVSCDGVDPDLFGAAPRYPLMDRFEV---YFRIQDLEMPQGRMHRVGLSGDNYL 559  
QY 549 RSKSGSLYVAICNMHQFIDEEPWFE-----KQVFPFHPPLRYREPVLKFDOSGL 600  
DB 560 RSPGRLRAALDRFRDMQVRCDFECENLYSADDQDAPSLDEEV-PEEPLLP-GTGI 617  
QY 601 VLNDVCKPSPESDFCLKVEAAVILGATGPADSQHE-----SQHGG 640  
DB 618 VKRAPLVRE-PSQACLAIDLPLVGEEGAIAVAKLEPHLQPRGQAPQPLHTLVLAABEGA 676  
QY 641 LDQDGEARPALDGA---ALQ-----PLLTVKAGSPDMRDSGIYDSSVPSSESLP 691  
DB 677 LVAAVEPGLADGAARLALAGEACPLGSPGAG-----RNSVLF---LPVDPEDSP 727  
QY 692 LMESLTDQETSSLESYSSSSGLGEEPPALPSKLLSSGCKADLGC 740  
DB 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAGGC 768

## RESULT 14

US-09-874-503-12

; Sequence 12, Application US/09874503

; Patent No. US20020177188A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Jian

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Li, Hanzhong

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Hymowitz, Sarah G.

; APPLICANT: Tumas, Daniel

; APPLICANT: Starovasanik, Menno

; APPLICANT: Vanden, Richard

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Yansura, Daniel

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

; FILE REFERENCE: P1381R1P3(US)

; CURRENT APPLICATION NUMBER: US/09/874,503

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/253,646

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 60/244,072

; PRIOR FILING DATE: 2000-10-26

PRIOR APPLICATION NUMBER: US 60/242,837  
 PRIOR FILING DATE: 2000-10-24  
 PRIOR APPLICATION NUMBER: US 60/175,481  
 PRIOR FILING DATE: 2000-01-11  
 PRIOR APPLICATION NUMBER: US 60/191,007  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: US 60/213,807  
 PRIOR FILING DATE: 2000-06-22  
 PRIOR APPLICATION NUMBER: US 60/172,096  
 PRIOR FILING DATE: 1999-12-23  
 PRIOR APPLICATION NUMBER: US 60/138,387  
 PRIOR FILING DATE: 1999-06-09  
 PRIOR APPLICATION NUMBER: US 60/134,287  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: US 60/131,022  
 PRIOR FILING DATE: 1999-04-26  
 PRIOR APPLICATION NUMBER: US 60/130,232  
 PRIOR FILING DATE: 1999-04-21  
 PRIOR APPLICATION NUMBER: US 60/113,621  
 PRIOR FILING DATE: 1998-12-23  
 PRIOR APPLICATION NUMBER: US 60/085,579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: US 09/854,208  
 PRIOR FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: US 09/854,280  
 PRIOR FILING DATE: 2001-05-20  
 PRIOR APPLICATION NUMBER: US 09/816,744  
 PRIOR FILING DATE: 2001-03-22  
 PRIOR APPLICATION NUMBER: US 09/747,259  
 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: US 09/644,848  
 PRIOR FILING DATE: 2000-08-22  
 PRIOR APPLICATION NUMBER: US 09/380,142  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: US 09/380,138  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: US 09/311,832  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: US PCT/US01/06520  
 PRIOR FILING DATE: 2001-02-28  
 PRIOR APPLICATION NUMBER: US PCT/US00/34956  
 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: US PCT/US00/32678  
 PRIOR FILING DATE: 2000-12-01  
 PRIOR APPLICATION NUMBER: US PCT/US00/30873  
 PRIOR FILING DATE: 2000-11-10  
 PRIOR APPLICATION NUMBER: US PCT/US00/23328  
 PRIOR FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: US PCT/US00/15264  
 PRIOR FILING DATE: 2000-06-02  
 PRIOR APPLICATION NUMBER: US PCT/US00/07532  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: US PCT/US00/05841  
 PRIOR FILING DATE: 2000-03-02  
 PRIOR APPLICATION NUMBER: US PCT/US00/05601  
 PRIOR FILING DATE: 2000-03-01  
 PRIOR APPLICATION NUMBER: US PCT/US00/04341  
 PRIOR FILING DATE: 2000-02-18  
 PRIOR APPLICATION NUMBER: US PCT/US99/31274  
 PRIOR FILING DATE: 1999-12-30  
 PRIOR APPLICATION NUMBER: US PCT/US99/10733  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: US PCT/US99/05028  
 PRIOR FILING DATE: 1999-03-08  
 NUMBER OF SEQ ID NOS: 39  
 SEQ ID NO 12  
 LENGTH: 502  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-09-874-503-12

Query Match 3.43; Score 135.5; DB 9; Length 502;  
 Best Local Similarity 20.14; Pred. No. 0.0046;

Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps 14;  
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 QY 262 -----KQOTTE-----TTSCILLQNVSPGYIIELVDDTNTTRVMHYALKPVHSPMAGPIR 313  
 Db 184 ITACKNEETVEVNTFTPL-----GNRYMALIQHSTI-----IGFSQVFPFHOKOT 231  
 QY 314 AVAITVPLWISAFATL-----FTVMCKRKKQOENIYSHLDESESS 355  
 Db 232 RASVIVPTVGDSEGNATVQLTPYFTGSCDIRHKTGVILC-----POTGVPPFLDNNSKPG 288  
 QY 356 TTTAAL-----PRELR-----PRKRVLCYSSKDGQNHMN 386  
 Db 289 GWLPLLLSLVATWVLVAGIYLMWHERIKKTSFTTTLLPPIKVLVVPSEICFHH-- 346  
 QY 387 VVOCEFAFLQDFCCEVALDWDGSLCREGQRENVIOKIHESQFIIVGSKGMYFVDK 446  
 Db 347 TICYTEFLQNHCRSEVILEKWKKKIAEMGPVQMLATOKKAADKVVFLLSNDVNSVCDG 406  
 QY 447 KNYKHGGGRGSGKGLFVAVSAIAEKLRQAKQSSAALSFKFIATVYFDYSCSDVPGL 506  
 Db 407 TCRSEGSFSENQ-DLFPALNLFCSDLR-----SQIHLHKYVVVYFREDTKDYNAL 460  
 QY 507 DLSTKRYLMDNLPQLCSHL 525  
 Db 461 SVCPRYHLMKDATAFCAEL 479

RESULT 15  
 US-10-000-157-12  
 Sequence 12, Application US/10000157  
 Publication No. US20020182673A1  
 GENERAL INFORMATION:  
 APPLICANT: Chen, Jian  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul L.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin  
 APPLICANT: Li, Hanzhong  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Hymowitz, Sarah  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Starovasinik, Melissa  
 APPLICANT: VanLookeren, Menno  
 APPLICANT: Vandlen, Richard  
 APPLICANT: Matanabe, Colin  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William  
 APPLICANT: Yansura, Daniel  
 TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
 FILE REFERENCE: P1381R1C1P4(US)  
 CURRENT APPLICATION NUMBER: US/10/000,157  
 CURRENT FILING DATE: 2001-10-30  
 PRIOR APPLICATION NUMBER: 60/085579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/113621  
 PRIOR FILING DATE: 1998-12-23  
 PRIOR APPLICATION NUMBER: 60/130232  
 PRIOR FILING DATE: 1999-04-21  
 PRIOR APPLICATION NUMBER: 60/131022  
 PRIOR FILING DATE: 1999-04-26  
 PRIOR APPLICATION NUMBER: 60/134287  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: 60/138387  
 PRIOR FILING DATE: 1999-06-09  
 PRIOR APPLICATION NUMBER: 60/172096  
 PRIOR FILING DATE: 1999-12-23  
 PRIOR APPLICATION NUMBER: 60/175481

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LENGTH: 502.
TYPE: PRT
ORGANISM: Homo Sapien
US-10-000-157-12

Query Match      3.4%; Score 135.5; DB 9; Length 502;
Best Local Similarity 20.1%; Pred. No. 0.0046;
Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps

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Db 143 NANNEDGFSMSVNETSPCCLDH-----IMKTK-----KCKVKAGSLMDPN 183
QY 262 -----KOEOTTE---TTSCLLNQVSPGDYIELVDVDTNTRKVMHYALKPVHSPWAGPIR 313
Db 184 ITACKNMEETVEVNTTPTL-----GNRYMALIQHSTI-----IGFSQVFEPHOKKOT 231
QY 314 AVAIVTPLVVISAEATL-----FTVMCRKKQOBSNIVSHLDESSESS 355
Db 232 RASVIVPTVDESGATVQLTPTPTCGSDCIIRKGTVILC---PQTGYVFPPLDNKSKPG 288
QY 356 TYTAAL-----PRELR-----PRPKVFLCYSSKOGQNHAN 386
Db 289 GWLPLLLLSLLVATVWLVAGIYVLAHREIRIKTSPSTTLLPIKVLVYVSEICPHH-- 346
QY 387 VVQCFAYVLDQFCGEVALDWDIEDSLCREGORENVQIKIHESQFIIVVCSGKHKYEVDK 446
Db 347 TICVYTEFLQHCRESVILEKWKOKKIAEMGPVQMLATQKAAKDKVFLLSNDVNSVCDG 406
QY 447 KNYKHKGGRGSGKEFLPVAVNSIAERKLQAKOSSNAALSKEIAYFYDSCGDVPGL 506
Db 407 TCGSKSGSPSENSQ-DLPLAFNLFCSDLR-----SQIHLHKYVVVYFREIDTKDDYNAL 460
QY 507 DLSTKYRLMDNLNLPOLCSHL 525
Db 461 SVCPKHYLMKDATAFACBL 479

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Job time : 28 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

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Run on: May 6, 2003, 13:42:46 ; Search time 153 Seconds  
(without alignments)  
3173.098 Million cell updates/sec

Title: US-09-912-157-2

Perfect score: 4013

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Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	3901	97.2	738	21	US-09-724-460-2
5	3901	97.2	738	22	US-09-809-567-2
6	3901	97.2	738	26	US-10-216-156-2

7	3835.5	95.6	738	22	US-09-863-818A-10	Sequence 10, Appl
8	3708	92.4	728	25	US-10-104-047-3399	Sequence 3399, Ap
9	3703	92.3	728	21	US-09-747-259-18	Sequence 18, Appl
10	3703	92.3	728	22	US-09-816-744-18	Sequence 18, Appl
11	3703	92.3	728	22	US-09-874-503-18	Sequence 18, Appl
12	3703	92.3	728	23	US-09-808-827A-18	Sequence 18, Appl
13	3703	92.3	728	23	US-09-808-827A-18	Sequence 18, Appl
14	3703	92.3	728	24	US-10-000-157-18	Sequence 18, Appl
15	3387	84.4	739	23	US-09-912-157-12	Sequence 12, Appl
16	3176	79.1	595	1	PCT-US02-15899-16	Sequence 16, Appl
17	3170	79.0	595	20	US-09-641-377-617	Sequence 617, App
18	1976	49.2	435	21	US-09-758-472-7594	Sequence 7594, Ap
19	1976	49.2	435	26	US-10-235-926-7594	Sequence 7594, Ap
20	312	7.8	810	21	US-09-724-460-3	Sequence 3, Appl1
21	312	7.8	810	22	US-09-809-567-3	Sequence 3, Appl1
22	312	7.8	810	26	US-10-216-156-3	Sequence 3, Appl1
23	312	7.8	866	1	PCT-US97-21451-4	Sequence 4, Appl1
24	312	7.8	866	18	US-09-488-728-4	Sequence 4, Appl1
25	312	7.8	866	19	US-09-549-679-10	Sequence 10, Appl
26	312	7.8	866	21	US-09-778-971-9	Sequence 9, Appl1
27	312	7.8	866	24	US-10-033-522-1	Sequence 1, Appl1
28	312	7.8	866	26	US-10-207-655-107	Sequence 107, App
29	306	7.6	864	1	PCT-US97-21451-2	Sequence 2, Appl1
30	306	7.6	864	18	US-09-488-728-2	Sequence 2, Appl1
31	306	7.6	864	19	US-09-549-679-2	Sequence 2, Appl1
32	271.5	6.8	539	21	US-09-723-232-3	Sequence 3, Appl1
33	271.5	6.8	539	22	US-09-810-927B-3	Sequence 3, Appl1
34	253.5	6.3	284	20	US-09-641-377-618	Sequence 618, App
35	232.5	5.8	207	22	US-09-863-818A-19	Sequence 19, Appl
36	222	5.5	208	22	US-09-863-818A-20	Sequence 20, Appl
37	139	3.5	453	27	US-09-612-601-2	Sequence 815, App
38	135.5	3.4	238	20	US-09-469-099-106	Sequence 106, App
39	135.5	3.4	385	18	US-09-599-360B-106	Sequence 106, App
40	135.5	3.4	385	19	US-09-723-232-7	Sequence 7, Appl1
41	135.5	3.4	385	21	US-09-810-927B-7	Sequence 7, Appl1
42	135.5	3.4	476	16	US-09-266-406-31	Sequence 31, Appl
43	135.5	3.4	485	16	US-09-266-406-12	Sequence 12, Appl
44	135.5	3.4	485	16	US-09-266-406-8	Sequence 8, Appl1
45	135.5	3.4	488	16	US-09-266-406-8	Sequence 8, Appl1

## ALIGNMENTS

## RESULT 1

US-09-912-157-2  
; Sequence 2, Application US/09912157  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Kuestner, Rolf E.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: Human Cytokine Receptor  
; FILE REFERENCE: 00-49  
; CURRENT APPLICATION NUMBER: US/09/912,157  
; CURRENT FILING DATE: 2001-07-23  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 753  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-912-157-2

Query Match 100.0%; Score 4013; DB 23; Length 753;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAPWLQCSVFFTVNACLSGSLAVALAAGSGRAGDTCGRMKAAARPLCVANEGVGP 60  
Db 1 MAPWLQCSVFFTVNACLSGSLAVALAAGSGRAGDTCGRMKAAARPLCVANEGVGP 60  
QY 61 ASRNSGLNITFKYDNCITLAPVGVKHIADONITTSOYACHDOQVAVTILWSPGALGIE 120  
|||||



Db 61 ASRNSGLNITFKYDNCNTTYLNPVGRHVIAADQNTITISQYACHDOQAVTILWSPGALGIE 120  
 QY 121 FLKGRVILEELKSEGROCOQILKADPKQLASSFKRTGMSOPFLNMFETDYFVKVVPF 180  
 Db 121 FLKGRVILEELKSEGROCOQILKADPKQLASSFKRTGMSOPFLNMFETDYFVKVVPF 180  
 QY 181 PSIKNESNYHPFFRTRACDLILQDPNKLACKPFWKPRNLNLSQHSQDMQVSPDHAPNFG 240  
 Db 181 PSIKNESNYHPFFRTRACDLILQDPNKLACKPFWKPRNLNLSQHSQDMQVSPDHAPNFG 240  
 QY 241 FRFFYLHLKHEGPPFRKTKCKOBTETTSCLLQNSPGDYIIELVDDTNTTRKVMHYA 300  
 Db 241 FRFFYLHLKHEGPPFRKTKCKOBTETTSCLLQNSPGDYIIELVDDTNTTRKVMHYA 300  
 QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCKKQOENIYSHLDEESSESSTYTA 360  
 Db 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCKKQOENIYSHLDEESSESSTYTA 360  
 QY 361 LPRERLRPRKVFELCYSSKQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420  
 Db 361 LPRERLRPRKVFELCYSSKQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420  
 QY 421 WVIQIHESQFIIVVCSKGMKVFVDKKNYKHGGSGKGEFLVAVSAIAEKLROAKQ 480  
 Db 421 WVIQIHESQFIIVVCSKGMKVFVDKKNYKHGGSGKGEFLVAVSAIAEKLROAKQ 480  
 QY 481 SSSAALSXFIATVFDYSCBQVPGILDSTKYRLMDNLPLQCSHLHSDHGLQEPGQHTR 540  
 Db 481 SSSAALSXFIATVFDYSCBQVPGILDSTKYRLMDNLPLQCSHLHSDHGLQEPGQHTR 540  
 QY 541 QGSRNRYFRSKGSRSLVAICNMHOFIDEPDMFEKQFVFPFPPPLRYREPVLKFDGSL 600  
 Db 541 QGSRNRYFRSKGSRSLVAICNMHOFIDEPDMFEKQFVFPFPPPLRYREPVLKFDGSL 600  
 QY 601 VLNDVCKPSPEDCLKVEAAYLGATGPADSOHESQHGGLQDGEARPAALDGSAALOPL 660  
 Db 601 VLNDVCKPSPEDCLKVEAAYLGATGPADSOHESQHGGLQDGEARPAALDGSAALOPL 660  
 QY 661 LHTVAGSPDMPSRDSGIYDSSVSPSSLSPLMEGLSTDTQETSSLSVESSSSGLGEE 720  
 Db 661 LHTVAGSPDMPSRDSGIYDSSVSPSSLSPLMEGLSTDTQETSSLSVESSSSGLGEE 720  
 QY 721 PPALPSKLLSSGCKADLGRSYTDELHVAAPL 753  
 Db 721 PPALPSKLLSSGCKADLGRSYTDELHVAAPL 753

## RESULT 2

US-09-912-157-5

; Sequence 5, Application US/09912157

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/09/912,157

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 753

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-912-157-5

Query Match

Best Local Similarity 99.8%; Score 4003; DB 23; Length 753;

Matches 751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAPQLQCSVFTTVACNLGSQLAVAGSGSRGARGADTCGRWKAARPRCLVCANEGVGP 60

Db 1 MAPQLQCSVFTTVACNLGSQLAVAGSGSRGARGADTCGRWKAARPRCLVCANEGVGP 60

QY 61 ASRNSGLNITFKYDNCNTTYLNPVGRHVIAADQNTITISQYACHDOQAVTILWSPGALGIE 120  
 Db 61 ASRNSGLNITFKYDNCNTTYLNPVGRHVIAADQNTITISQYACHDOQAVTILWSPGALGIE 120  
 QY 121 FLKGRVILEELKSEGROCOQILKADPKQLASSFKRTGMSOPFLNMFETDYFVKVVPF 180  
 Db 121 FLKGRVILEELKSEGROCOQILKADPKQLASSFKRTGMSOPFLNMFETDYFVKVVPF 180  
 QY 181 PSIKNESNYHPFFRTRACDLILQDPNKLACKPFWKPRNLNLSQHSQDMQVSPDHAPNFG 240  
 Db 181 PSIKNESNYHPFFRTRACDLILQDPNKLACKPFWKPRNLNLSQHSQDMQVSPDHAPNFG 240  
 QY 241 FRFFYLHLKHEGPPFRKTKCKOBTETTSCLLQNSPGDYIIELVDDTNTTRKVMHYA 300  
 Db 241 FRFFYLHLKHEGPPFRKTKCKOBTETTSCLLQNSPGDYIIELVDDTNTTRKVMHYA 300  
 QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCKKQOENIYSHLDEESSESSTYTA 360  
 Db 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCKKQOENIYSHLDEESSESSTYTA 360  
 QY 361 LPRERLRPRKVFELCYSSKQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420  
 Db 361 LPRERLRPRKVFELCYSSKQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420  
 QY 421 WVIQIHESQFIIVVCSKGMKVFVDKKNYKHGGSGKGEFLVAVSAIAEKLROAKQ 480  
 Db 421 WVIQIHESQFIIVVCSKGMKVFVDKKNYKHGGSGKGEFLVAVSAIAEKLROAKQ 480  
 QY 481 SSSAALSXFIATVFDYSCBQVPGILDSTKYRLMDNLPLQCSHLHSDHGLQEPGQHTR 540  
 Db 481 SSSAALSXFIATVFDYSCBQVPGILDSTKYRLMDNLPLQCSHLHSDHGLQEPGQHTR 540  
 QY 541 QGSRNRYFRSKGSRSLVAICNMHOFIDEPDMFEKQFVFPFPPPLRYREPVLKFDGSL 600  
 Db 541 QGSRNRYFRSKGSRSLVAICNMHOFIDEPDMFEKQFVFPFPPPLRYREPVLKFDGSL 600  
 QY 601 VLNDVCKPSPEDCLKVEAAYLGATGPADSOHESQHGGLQDGEARPAALDGSAALOPL 660  
 Db 601 VLNDVCKPSPEDCLKVEAAYLGATGPADSOHESQHGGLQDGEARPAALDGSAALOPL 660  
 QY 661 LHTVAGSPDMPSRDSGIYDSSVSPSSLSPLMEGLSTDTQETSSLSVESSSSGLGEE 720  
 Db 661 LHTVAGSPDMPSRDSGIYDSSVSPSSLSPLMEGLSTDTQETSSLSVESSSSGLGEE 720  
 QY 721 PPALPSKLLSSGCKADLGRSYTDELHVAAPL 753  
 Db 721 PPALPSKLLSSGCKADLGRSYTDELHVAAPL 753

## RESULT 3

US-09-912-157-8

; Sequence 8, Application US/09912157

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/09/912,157

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 739

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-912-157-8

Query Match

Best Local Similarity 97.8%; Score 3925; DB 23; Length 739;

Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 MAPWQLCSVFTVNAACLSQLAAGGSRGADTCGRMAAARPRLCVANEGVGP 60  
DB 1 MAPWQLCSVFTVNAACLSQLAAGGSRGADTCGRMAAARPRLCVANEGVGP 46  
QY 61 ASRNSGLNITFKYDNCITTLNPKVGHVIAADQNTISQACHDOVAVTILWSPGALGIE 120  
DB 47 ASRNSGLNITFKYDNCITTLNPKVGHVIAADQNTISQACHDOVAVTILWSPGALGIE 106  
QY 121 FLKFRVILELKSREGROCOQILKDPKOLNSFKRTGMSQPFNNKKTETDFYKVVVPF 180  
DB 107 FLKFRVILELKSREGROCOQILKDPKOLNSFKRTGMSQPFNNKKTETDFYKVVVPF 166  
QY 181 PSIKNESNYHPEFFTRACDLLOPDNLACKPFWKPRNLNISQSGDMQVSDHAPHNFG 240  
DB 167 PSIKNESNYHPEFFTRACDLLOPDNLACKPFWKPRNLNISQSGDMQVSDHAPHNFG 226  
QY 241 FRFFYLKHLKHEGPKRTCKOBTETTSCLLQNVSPGDYIELVDVDTNTRKVMHYA 300  
DB 227 FRFFYLKHLKHEGPKRTCKOBTETTSCLLQNVSPGDYIELVDVDTNTRKVMHYA 286  
QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCRKQOENIYSHLDESESESTYTA 360  
DB 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCRKQOENIYSHLDESESESTYTA 346  
QY 361 LPRERLRPRKPVLCYSSKOGQNHMNVQCFAYFLQDFCCEVALDLWEDFSLCREGORE 420  
DB 347 LPRERLRPRKPVLCYSSKOGQNHMNVQCFAYFLQDFCCEVALDLWEDFSLCREGORE 406  
QY 421 WYIQRHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGFELFLVAVSAIAEKLRQAK 480  
DB 407 WYIQRHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGFELFLVAVSAIAEKLRQAK 466  
QY 481 SSSAALSKEFIIVVCSKGMKYFVDKKNYKHGGGSGKGFELFLVAVSAIAEKLRQAK 540  
DB 467 SSSAALSKEFIIVVCSKGMKYFVDKKNYKHGGGSGKGFELFLVAVSAIAEKLRQAK 526  
QY 541 QGSRNRYFRSKGRSLIYAICNMHOFIDEEPDMFEKQFVFPFPPPLRYREPVLKFDGSL 600  
DB 527 QGSRNRYFRSKGRSLIYAICNMHOFIDEEPDMFEKQFVFPFPPPLRYREPVLKFDGSL 586  
QY 601 VLNDVCKPSPESDFCLKVEAAVLGATGPADSOHSGHGLDQGEARPDGSAALQPL 660  
DB 587 VLNDVCKPSPESDFCLKVEAAVLGATGPADSOHSGHGLDQGEARPDGSAALQPL 646  
QY 661 LHTVAKGSPDMPRDGIYDSSVSPSELSPLMEGLSTDTQTTSSITSVSSSSGLGEE 720  
DB 647 LHTVAKGSPDMPRDGIYDSSVSPSELSPLMEGLSTDTQTTSSITSVSSSSGLGEE 706  
QY 721 PPALPSKLLSSGSKADLCGRSYTDELHAPV 753  
DB 707 PPALPSKLLSSGSKADLCGRSYTDELHAPV 739

## RESULT 4

US-09-724-460-2

; Sequence 2, Application US/09724460

; GENERAL INFORMATION:

; APPLICANT: Jing, Shuqian

; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof

; FILE REFERENCE: 01017/36916

; CURRENT APPLICATION NUMBER: US/09/724,460

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 60/189,816

; PRIOR FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 738

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-460-2

Query Match

97.2%; Score 3901; DB 21;

Length 738;

Best Local Similarity 97.6%; Pred. No. 0;  
Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 1 MAPWQLCSVFTVNAACLSQLAAGGSRGADTCGRMAAARPRLCVANEGVGP 60

DB 1 MAPWQLCSVFTVNAACLSQLAAGGSRGADTCGRMAAARPRLCVANEGVGP 46

QY 61 ASRNSGLNITFKYDNCITTLNPKVGHVIAADQNTISQACHDOVAVTILWSPGALGIE 120

DB 47 ASRNSGLNITFKYDNCITTLNPKVGHVIAADQNTISQACHDOVAVTILWSPGALGIE 106

QY 121 FLKFRVILELKSREGROCOQILKDPKOLNSFKRTGMSQPFNNKKTETDFYKVVVPF 180

DB 107 FLKFRVILELKSREGROCOQILKDPKOLNSFKRTGMSQPFNNKKTETDFYKVVVPF 166

QY 181 PSIKNESNYHPEFFTRACDLLOPDNLACKPFWKPRNLNISQSGDMQVSDHAPHNFG 240

DB 167 PSIKNESNYHPEFFTRACDLLOPDNLACKPFWKPRNLNISQSGDMQVSDHAPHNFG 226

QY 241 FRFFYLKHLKHEGPKRTCKOBTETTSCLLQNVSPGDYIELVDVDTNTRKVMHYA 300

DB 227 FRFFYLKHLKHEGPKRTCKOBTETTSCLLQNVSPGDYIELVDVDTNTRKVMHYA 286

QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCRKQOENIYSHLDESESESTYTA 360

DB 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCRKQOENIYSHLDESESESTYTA 346

QY 361 LPRERLRPRKPVLCYSSKOGQNHMNVQCFAYFLQDFCCEVALDLWEDFSLCREGORE 420

DB 347 LPRERLRPRKPVLCYSSKOGQNHMNVQCFAYFLQDFCCEVALDLWEDFSLCREGORE 406

QY 421 WYIQRHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGFELFLVAVSAIAEKLRQAK 480

DB 407 WYIQRHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGFELFLVAVSAIAEKLRQAK 466

QY 481 SSSAALSKEFIIVVCSKGMKYFVDKKNYKHGGGSGKGFELFLVAVSAIAEKLRQAK 540

DB 467 SSSAALSKEFIIVVCSKGMKYFVDKKNYKHGGGSGKGFELFLVAVSAIAEKLRQAK 526

QY 541 QGSRNRYFRSKGRSLIYAICNMHOFIDEEPDMFEKQFVFPFPPPLRYREPVLKFDGSL 600

DB 527 QGSRNRYFRSKGRSLIYAICNMHOFIDEEPDMFEKQFVFPFPPPLRYREPVLKFDGSL 586

QY 601 VLNDVCKPSPESDFCLKVEAAVLGATGPADSOHSGHGLDQGEARPDGSAALQPL 660

DB 587 VLNDVCKPSPESDFCLKVEAAVLGATGPADSOHSGHGLDQGEARPDGSAALQPL 646

QY 661 LHTVAKGSPDMPRDGIYDSSVSPSELSPLMEGLSTDTQTTSSITSVSSSSGLGEE 720

DB 647 LHTVAKGSPDMPRDGIYDSSVSPSELSPLMEGLSTDTQTTSSITSVSSSSGLGEE 706

QY 721 PPALPSKLLSSGSKADLCGRSYTDELHAPV 752

DB 707 PPALPSKLLSSGSKADLCGRSYTDELHAPV 738

## RESULT 5

US-09-809-567-2

; Sequence 2, Application US/09809567

; GENERAL INFORMATION:

; APPLICANT: Jing, Shuqian

; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof

; FILE REFERENCE: 01017/36916A

; CURRENT APPLICATION NUMBER: US/09/809,567

; CURRENT FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: 09/724,460

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 60/189,816

; PRIOR FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 738

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-809-567-2

Query Match: 97.24; Score 3901; DB 22; Length 738;  
Best Local Similarity: 97.64; Pred. No. 0;  
Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 1 MAPWLQLCVFFFTVNAACLSQSLAVAGGSGRARGADTCGRWMAAARPRLCVANEGVGP 60  
DB 1 MAPWLQLCVFFFTVNAACLSQSLAVAGGSGRARGADTCGRWMAAARPRLCVANEGVGP 60  
QY 61 ASRNSGLYNITFKYDNCCTTILNPVGHVIAADQNTISQYACHDOVAVTILSPGALGIE 120  
DB 47 ASRNSGLYNITFKYDNCCTTILNPVGHVIAADQNTISQYACHDOVAVTILSPGALGIE 106  
QY 121 FLKGRFVILEELKSEGRQCOOLILKDPKOLNSFKRTGMSOPFLNKKFTDYFKVVPF 180  
DB 107 FLKGRFVILEELKSEGRQCOOLILKDPKOLNSFKRTGMSOPFLNKKFTDYFKVVPF 166  
QY 181 PSIKNESNTHFFTRACDQLLPDLNACKPFWKPRNLISQSGDMQVSPDHAPHNG 240  
DB 167 PSIKNESNTHFFTRACDQLLPDLNACKPFWKPRNLISQSGDMQVSPDHAPHNG 226  
QY 241 FRFFLHLKHEGPFRTCKQEQTTTSCLLQNVSPGDIIELVDDTNTTRKVMHYA 300  
DB 227 FRFFLHLKHEGPFRTCKQEQTTTSCLLQNVSPGDIIELVDDTNTTRKVMHYA 286  
QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTA 360  
DB 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTA 346  
QY 361 LPRERLRPRKPVLCYSSKQGNHNVVOCFAIFLODFCGCEVALDLWEDFSLCREGORE 420  
DB 347 LPRERLRPRKPVLCYSSKQGNHNVVOCFAIFLODFCGCEVALDLWEDFSLCREGORE 406  
QY 421 WYQIKHESQFIIVVCSKGMKYFVDKKNYKHGGSGGSGKGEFLVAVSAIAEKLRAQK 480  
DB 407 WYQIKHESQFIIVVCSKGMKYFVDKKNYKHGGSGGSGKGEFLVAVSAIAEKLRAQK 466  
QY 481 SSSAALSKEFIIVVCSKGMKYFVDKKNYKHGGSGGSGKGEFLVAVSAIAEKLRAQK 540  
DB 467 SSSAALSKEFIIVVCSKGMKYFVDKKNYKHGGSGGSGKGEFLVAVSAIAEKLRAQK 526  
QY 541 QGSRNRYFRSKGRSLYVAICNHQFIDEEDPWFKEQFVPPHPPPLRYEPVLEKFDGSL 600  
DB 527 QGSRNRYFRSKGRSLYVAICNHQFIDEEDPWFKEQFVPPHPPPLRYEPVLEKFDGSL 586  
QY 601 VLNDVMCKPGPESDFCLKVEAPVLGATGPADSOHESQHGGLDQGEARPALDGSAAALQPL 660  
DB 587 VLNDVMCKPGPESDFCLKVEAPVLGATGPADSOHESQHGGLDQGEARPALDGSAAALQPL 646  
QY 661 LHTVAGSPDMPRDGIYDSSVPSSELSPLMEGLSTDQTTSSLTESVSSSSGLGEE 720  
DB 647 LHTVAGSPDMPRDGIYDSSVPSSELSPLMEGLSTDQTTSSLTESVSSSSGLGEE 706  
QY 721 PPALPSKLLSSGCKADLCGRSYTDELHAPV 752  
DB 707 PPALPSKLLSSGCKADLCGRSYTDELHAPV 738

## RESULT 6

US-10-216-156-2

Sequence 2, Application US/10216156

GENERAL INFORMATION:

APPLICANT: Jing, Shuguan

TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof

FILE REFERENCE: 01017/36916A

CURRENT APPLICATION NUMBER: US/10/216,156

CURRENT FILING DATE: 2002-08-08

PRIOR APPLICATION NUMBER: US/09/809,567

PRIOR FILING DATE: 2001-03-15

PRIOR APPLICATION NUMBER: 09/724,460

PRIOR FILING DATE: 2000-11-28;  
PRIOR APPLICATION NUMBER: 60/189,816  
PRIOR FILING DATE: 2000-03-16;  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 738  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-216-156-2

Query Match: 97.24; Score 3901; DB 26; Length 738;

Best Local Similarity: 97.64; Pred. No. 0;

Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 1 MAPWLQLCVFFFTVNAACLSQSLAVAGGSGRARGADTCGRWMAAARPRLCVANEGVGP 60  
DB 1 MAPWLQLCVFFFTVNAACLSQSLAVAGGSGRARGADTCGRWMAAARPRLCVANEGVGP 46  
QY 61 ASRNSGLYNITFKYDNCCTTILNPVGHVIAADQNTISQYACHDOVAVTILSPGALGIE 120  
DB 47 ASRNSGLYNITFKYDNCCTTILNPVGHVIAADQNTISQYACHDOVAVTILSPGALGIE 106  
QY 121 FLKGRFVILEELKSEGRQCOOLILKDPKOLNSFKRTGMSOPFLNKKFTDYFKVVPF 180  
DB 107 FLKGRFVILEELKSEGRQCOOLILKDPKOLNSFKRTGMSOPFLNKKFTDYFKVVPF 166  
QY 181 PSIKNESNTHFFTRACDQLLPDLNACKPFWKPRNLISQSGDMQVSPDHAPHNG 240  
DB 167 PSIKNESNTHFFTRACDQLLPDLNACKPFWKPRNLISQSGDMQVSPDHAPHNG 226  
QY 241 FRFFLHLKHEGPFRTCKQEQTTTSCLLQNVSPGDIIELVDDTNTTRKVMHYA 300  
DB 227 FRFFLHLKHEGPFRTCKQEQTTTSCLLQNVSPGDIIELVDDTNTTRKVMHYA 286  
QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTA 360  
DB 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTA 346  
QY 361 LPRERLRPRKPVLCYSSKQGNHNVVOCFAIFLODFCGCEVALDLWEDFSLCREGORE 420  
DB 347 LPRERLRPRKPVLCYSSKQGNHNVVOCFAIFLODFCGCEVALDLWEDFSLCREGORE 406  
QY 421 WYQIKHESQFIIVVCSKGMKYFVDKKNYKHGGSGGSGKGEFLVAVSAIAEKLRAQK 480  
DB 407 WYQIKHESQFIIVVCSKGMKYFVDKKNYKHGGSGGSGKGEFLVAVSAIAEKLRAQK 466  
QY 481 SSSAALSKEFIIVVCSKGMKYFVDKKNYKHGGSGGSGKGEFLVAVSAIAEKLRAQK 540  
DB 467 SSSAALSKEFIIVVCSKGMKYFVDKKNYKHGGSGGSGKGEFLVAVSAIAEKLRAQK 526  
QY 541 QGSRNRYFRSKGRSLYVAICNHQFIDEEDPWFKEQFVPPHPPPLRYEPVLEKFDGSL 600  
DB 527 QGSRNRYFRSKGRSLYVAICNHQFIDEEDPWFKEQFVPPHPPPLRYEPVLEKFDGSL 586  
QY 601 VLNDVMCKPGPESDFCLKVEAPVLGATGPADSOHESQHGGLDQGEARPALDGSAAALQPL 660  
DB 587 VLNDVMCKPGPESDFCLKVEAPVLGATGPADSOHESQHGGLDQGEARPALDGSAAALQPL 646  
QY 661 LHTVAGSPDMPRDGIYDSSVPSSELSPLMEGLSTDQTTSSLTESVSSSSGLGEE 720  
DB 647 LHTVAGSPDMPRDGIYDSSVPSSELSPLMEGLSTDQTTSSLTESVSSSSGLGEE 706  
QY 721 PPALPSKLLSSGCKADLCGRSYTDELHAPV 752  
DB 707 PPALPSKLLSSGCKADLCGRSYTDELHAPV 738

## RESULT 7

US-09-863-018A-10

Sequence 10, Application US/09863818A

GENERAL INFORMATION:

APPLICANT: Gorman, Daniel M.

## TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

FILE REFERENCE: D01170K  
 CURRENT APPLICATION NUMBER: US/09/863,818A  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/206,862  
 PRIOR FILING DATE: 2000-05-24  
 NUMBER OF SEQ ID NOS: 22  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 10  
 LENGTH: 738  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (18)..(18)  
 OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.  
 NAME/KEY: misc.feature  
 LOCATION: (26)..(26)  
 OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.  
 NAME/KEY: misc.feature  
 LOCATION: (109)..(109)  
 OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.  
 NAME/KEY: misc.feature  
 LOCATION: (120)..(120)  
 OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.  
 NAME/KEY: misc.feature  
 LOCATION: (134)..(134)  
 OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.  
 NAME/KEY: misc.feature  
 LOCATION: (8)..(8)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc.feature  
 LOCATION: (144)..(144)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc.feature  
 LOCATION: (170)..(170)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc.feature  
 LOCATION: (194)..(194)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc.feature  
 LOCATION: (442)..(442)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc.feature  
 LOCATION: (475)..(475)  
 OTHER INFORMATION: unknown amino  
 NAME/KEY: misc.feature  
 LOCATION: (519)..(519)  
 OTHER INFORMATION: unknown amino  
 US-09-863-818A-10

Query Match 95.6%; Score 3835.5; DB 22; Length 738;  
 Best Local Similarity 96.4%; Pred. No. 0;  
 Matches 726; Conservative 2; Mismatches 10; Indels 15; Gaps 2;  
 QY 1 MAPWLQCSVFTVNAACLSGSLAAGGSGRARGADTCGWKMAARPLCVANGVGP 60  
 DB 1 MAPWLQCSVFTVNAACLSGSLAAGGSGRARGADTCGWKMAARPLCVANGVGP 46  
 QY 61 ASNSGLNITFKYDNCNTYLNPGKHVIAADQNTISQYACHQDVAVTILWSPGALGIE 120  
 DB 47 ASNSGLNITFKYDNCNTYLNPGKHVIAADQNTISQYACHQDVAVTILWSPGALGIE 106  
 QY 121 FLKGFVILEELKSGRCQQLILKDPKQNSFKRTGMSOPFLNKKFETDVFVKVWPF 180  
 DB 107 FLKGFVILEELKSGRCQQLILKDPKQNSFKRTGMSOPFLNKKFETDVFVR-LSP 165  
 QY 181 PSIKNESNYHFFFTTRACDLILQPNLACKPFWKPRNINISQSGSDMOVSDFOHAPNFG 240  
 DB 166 SFIKNESNYHFFFTTRACDLILQPNLACKPFWKPRNINISQSGSDMOVSDFOHAPNFG 225  
 QY 241 FRFFYLHYKLHKGPPFKKTKCKQQTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300  
 DB FRFFYLHYKLHKGPPFKKTKCKQQTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 270

DB 226 FRFFYLHYKLHKGPPFKKTKCKQQTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 285  
 QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCKKQKQENIYSHLDESSSSTYTA 360  
 DB 286 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVCKKQKQENIYSHLDESSSSTYTA 345  
 QY 361 LPRERLRPRKVFICYSSKDGQNNHNVQCFAYFLQDFCGCEVALDLDWEDFSLCRGQRE 420  
 DB 346 LPRERLRPRKVFICYSSKDGQNNHNVQCFAYFLQDFCGCEVALDLDWEDFSLCRGQRE 405  
 QY 421 WYIQIHESQFIIVVCSKGMKVFVDKKNYKHGGGSGKGELEFLVSAIAEKLQAKQ 480  
 DB 406 WYIQIHESQFIIVVCSKGMKVFVDKKNYKHGGGSGKGELEFLVSAIAEKLQAKQ 465  
 QY 481 SSSAALSFIAYFDYSCGDVPGIILDLSTKYRLMDNLPQLCSHLHSDRHGLQEPQHTR 540  
 DB 466 SSSAALSFIAYFDYSCGDVPGIILDLSTKYRLMDNLPQLCSHLHSDRHGLQEPQHTR 525  
 QY 541 QGSRNRYFRSKGRSLVAICNNHQFIDEEDPWFQKVPFPPPLRYREPVLKEDSGL 600  
 DB 526 QGSRNRYFRSKGRSLVAICNNHQFIDEEDPWFQKVPFPPPLRYREPVLKEDSGL 585  
 QY 601 VLVNDVCKPGPESDFCLKVEAIVLGATGADSPQSHQSGHGLDQGEARPAALQPL 660  
 DB 586 VLVNDVCKPGPESDFCLKVEAIVLGATGADSPQSHQSGHGLDQGEARPAALQPL 645  
 QY 661 LHTVKAGSPDMRDSGIYDSSVPSSELSPLMEGLSTDTQETSSLTSESYSSSSGGEE 720  
 DB 646 LHTVKAGSPDMRDSGIYDSSVPSSELSPLMEGLSTDTQETSSLTSESYSSSSGGEE 705  
 QY 721 PPALPSKILLSSGCKADLGCSTYDELHAYAPL 753  
 DB 706 PPALPSKILLSSGCKADLGCSTYDELHAYAPL 738

## RESULT 8

US-10-104-047-3399  
 ; Sequence 3399, Application US/10104047  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HELIX RESEARCH INSTITUTE  
 ; TITLE OF INVENTION: Novel full length cDNA  
 ; FILE REFERENCE: H1-A0105  
 ; CURRENT APPLICATION NUMBER: US/10/104,047  
 ; CURRENT FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER:  
 ; PRIOR FILING DATE:  
 ; NUMBER OF SEQ ID NOS: 4096  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3399  
 ; LENGTH: 728  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-104-047-3399

Query Match 92.4%; Score 3708; DB 25; Length 728;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 696; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 56 BVGSPASRNSGLYNITFKYDNCNTYLNPGKHVIAADQNTISQYACHQDVAVTILWSPG 115  
 DB 31 QCVGSPASRNSGLYNITFKYDNCNTYLNPGKHVIAADQNTISQYACHQDVAVTILWSPG 90  
 QY 116 ALGIEFLKGFVILEELKSGRCQQLILKDPKQNSFKRTGMSOPFLNKKFETDVF 175  
 DB 91 ALGIEFLKGFVILEELKSGRCQQLILKDPKQNSFKRTGMSOPFLNKKFETDVF 150  
 QY 176 KVVPPPSIKNESNYHFFFTTRACDLILQPNLACKPFWKPRNINISQSGSDMOVSDFOH 235  
 DB 151 KVVPPPSIKNESNYHFFFTTRACDLILQPNLACKPFWKPRNINISQSGSDMOVSDFOH 210  
 QY 236 PHNFGFRFFYLHYKLHKGPPFKKTKCKQQTETTSCLLQNVSPGDYIIELVDDTNTTRK 295  
 DB 211 PHNFGFRFFYLHYKLHKGPPFKKTKCKQQTETTSCLLQNVSPGDYIIELVDDTNTTRK 270

QY 296 VHYALKVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDESS 355  
DB 271 VHYALKVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDESS 330  
QY 356 TYTAALPRELRPRKPVLCYSSKQOENIYSHLDESS 415  
DB 331 TYTAALPRELRPRKPVLCYSSKQOENIYSHLDESS 390  
QY 416 EGROENVIOKIHESOFIIVWC-SKGYEYVVKNYKKGGRSGSGELFLVAVSAIAEKL 475  
DB 391 EGROENVIOKIHESOFIIVWC-SKGYEYVVKNYKKGGRSGSGELFLVAVSAIAEKL 450  
QY 476 ROAKQSSAALSKFTAVYDFISCEGDPVGLDLSKTYRLMDNLPOLCSHLHSDHGLQEP 535  
DB 451 ROAKQSSAALSKFTAVYDFISCEGDPVGLDLSKTYRLMDNLPOLCSHLHSDHGLQEP 510  
QY 536 GOHTRGSRNTRFKSGRSYLYAICNMHOFIDEEPDMFEKOFVPHPPPLRYREPYLEK 595  
DB 511 GOHTRGSRNTRFKSGRSYLYAICNMHOFIDEEPDMFEKOFVPHPPPLRYREPYLEK 570  
QY 596 FDSGLVNDVMCKPGPESDFCLKVEAAVLGATGPADQSQHSQHGGLDQGEARALDQSA 655  
DB 571 FDSGLVNDVMCKPGPESDFCLKVEAAVLGATGPADQSQHSQHGGLDQGEARALDQSA 630  
QY 656 ALQPLHTVYKAGSPDMRDSGIYDSSVPSSELSPLMGLSTDTOTSSLSSES 715  
DB 631 ALQPLHTVYKAGSPDMRDSGIYDSSVPSSELSPLMGLSTDTOTSSLSSES 690  
QY 716 LGEEPPALPKSLSSGCKADLACRSYTDLHAYAPL 753  
DB 691 LGEEPPALPKSLSSGCKADLACRSYTDLHAYAPL 728

RESULT 9  
US-09-747-259-18  
; Sequence 18, Application US/09747259  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Chen, Jian  
; APPLICANT: Filaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Hillman, Kenneth  
; APPLICANT: Tumaq, Daniel  
; APPLICANT: VanLookeren, Menno  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William  
; APPLICANT: Yansura, Daniel  
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
; FILE REFERENCE: P1381R1C1P1(US)  
; CURRENT APPLICATION NUMBER: US/09/747,259  
; PRIOR FILING DATE: 2000-12-20  
; CURRENT APPLICATION NUMBER: US 09/311,832  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: US 60/172,096  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: PCT/US99/31274  
; PRIOR FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: US 60/175,481  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: PCT/US00/04341  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: US 60/191,007  
; PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: US 60/213,087  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 09/644,848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/242,837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: US 60/253,646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 18  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-747-259-18

Query Match 92.3%; Score 3703; DB 21; Length 728;  
Best Local Similarity 96.7%; Pred. No. 0;  
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RMKAAARPLCVAE-GVGPASRNSGLYNTFYKDYDNCYTLNPNVGVKHIADAQNTISQY 100  
DB 3 RASAGVPALFVSGEGVGPASRNSGLYNTFYKDYDNCYTLNPNVGVKHIADAQNTISQY 62  
QY 101 ACHDOVAVTILWSPGALGIEFLAGFRVILEELKSGROCOOLILKDPQLNSFKRTGME 160  
DB 63 ACHDOVAVTILWSPGALGIEFLAGFRVILEELKSGROCOOLILKDPQLNSFKRTGME 122  
QY 161 SQPFLNKFETDYFVKVVPFSPKSNSTHPTFRACDILLQDNLACKPFWKPRNLN 220  
DB 123 SQPFLNKFETDYFVKVVPFSPKSNSTHPTFRACDILLQDNLACKPFWKPRNLN 182  
QY 221 ISO-----HGSDMVSDHAPHNGFRFFVLYLHYLKLHKGFGFRKTKCKOQTT 267  
DB 183 ISOHSDMVSDHAPHNGFRFFVLYLHYLKLHKGFGFRKTKCKOQTT 242  
QY 268 ETTSCLLQNVSPGDIYIELVDDTNTTKVNHVYALPVPVSPWAGPIRAVAITVPLVVISAF 327  
DB 243 EMTSCLLQNVSPGDIYIELVDDTNTTKVNHVYALPVPVSPWAGPIRAVAITVPLVVISAF 302  
QY 328 ATLFTVMCRKQOENIYSHLDESSSESTYTAALPRELRPRKPVLCYSSKQOENHMY 387  
DB 303 ATLFTVMCRKQOENIYSHLDESSSESTYTAALPRELRPRKPVLCYSSKQOENHMY 362  
QY 388 VOCFAYFLQDCGCEVALDLDWEDFSLCRGQREWVIOKHESQFTIIVVCSKGMKYFVDDK 447  
DB 363 VOCFAYFLQDCGCEVALDLDWEDFSLCRGQREWVIOKHESQFTIIVVCSKGMKYFVDDK 422  
QY 448 NYKHGGGSGSGKGEFLVAVSAIAEKLROAKQSSAALSFIYFYDYSCEGDPVGLD 507  
DB 423 NYKHGGGSGSGKGEFLVAVSAIAEKLROAKQSSAALSFIYFYDYSCEGDPVGLD 482  
QY 508 LSTKYRLMDNLPOLCSHLHSDHGLQEPGOHTRGSRNTRFKSGRSYLYAICNMHOFI 567  
DB 483 LSTKYRLMDNLPOLCSHLHSDHGLQEPGOHTRGSRNTRFKSGRSYLYAICNMHOFI 542  
QY 568 DEEPDMFEKOFVPHPPPLRYREPYLEKFDLSGLVNDVMCKPGPESDFCLKVEAAVLGAT 627  
DB 543 DEEPDMFEKOFVPHPPPLRYREPYLEKFDLSGLVNDVMCKPGPESDFCLKVEAAVLGAT 602  
QY 628 GPADQSQHSQHGGLDQGEARALDQSAALQPLHTVYKAGSPDMRDSGIYDSSVPSSE 687  
DB 603 GPADQSQHSQHGGLDQGEARALDQSAALQPLHTVYKAGSPDMRDSGIYDSSVPSSE 662

QY 688 LSLPLMEGLSTDTQETSLTSSVSSGSGEPPALPSSKLLSSGCKADLCGRSYDEL 747  
Db 663 LSLPLMEGLSTDTQETSLTSSVSSGSGEPPALPSSKLLSSGCKADLCGRSYDEL 722  
QY 748 HAVAPL 753  
Db 723 HAVAPL 728  
RESULT 10  
US-09-816-744-18  
Sequence 18, Application US/09816744  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Tumas, Daniel  
APPLICANT: VanLookeren, Menno  
APPLICANT: Vandlen, Richard  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Yansura, Daniel  
FILE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381R1CIP2(US)  
CURRENT APPLICATION NUMBER: US/09/816,744  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 18  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-816-744-18

Query Match 92.38; Score 3703; DB 22; Length 728;  
Best Local Similarity: 96.78; Pred. No. 0;  
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;  
QY 42 RKMAARPLCVANE-GVGPASRNSGLYNITFKYDNCITLNPVKGKVIADAQNITISQY 100  
Db 3 RASASGVPAIFVSGGVGPASRNSGLYNITFKYDNCITLNPVKGKVIADAQNITISQY 62  
QY 101 ACHQVAVTILSPALGIEFLAGFRVILEELKSEGRQCOQILKDPKQLNSFKRTGME 160  
Db 63 ACHQVAVTILSPALGIEFLAGFRVILEELKSEGRQCOQILKDPKQLNSFKRTGME 122  
QY 161 SOPFLANKPETDYFKVYVPPPSIKNESYHPFFRTRACDILLQPDNLACKPFWKPRNLN 220  
Db 123 SOPFLANKPETDYFKVYVPPPSIKNESYHPFFRTRACDILLQPDNLACKPFWKPRNLN 182  
QY 221 ISQ-----HGSMDVSDHAPHNCFREFYLYLKLHKGFFRKTCKQEQTT 267  
Db 183 ISQSGDMQVSDHAPHGSMQVSDHAPHNCFREFYLYLKLHKGFFRKTCKQEQTT 242  
QY 268 ETTSCLLQNVSPGDIYIELVDVDTNTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAF 327  
Db 243 EMTSCLLQNVSPGDIYIELVDVDTNTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAF 302  
QY 328 ATLPTVCKRKKQENIYSHLDESESSSTYALPRERLRPRKPVFLCYSSKQCONHNV 387  
Db 303 ATLPTVCKRKKQENIYSHLDESESSSTYALPRERLRPRKPVFLCYSSKQCONHNV 362  
QY 388 VOCFAYFLQDFCGCEVALDWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKIFYDKK 447  
Db 363 VOCFAYFLQDFCGCEVALDWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKIFYDKK 422

QY 448 NYKHGGGGRSGKGEPLFVAVSAIAEKLRQAKOSSAALSXFIAYFYDYSCGEGVPCILD 507  
Db 423 NYKHGGGGRSGKGEPLFVAVSAIAEKLRQAKOSSAALSXFIAYFYDYSCGEGVPCILD 482  
QY 508 LSTKYRLMDNLPLQCSHLHSHRDHGLQEPGQHTROGSRNRNYFRSKSGRLVAICNMHQFI 567  
Db 483 LSTKYRLMDNLPLQCSHLHSHRDHGLQEPGQHTROGSRNRNYFRSKSGRLVAICNMHQFI 542  
QY 568 DEEPDWFEEKQVPPPHPPPLRYREPVLKFDGSLVLNDVMCKPGPESDPCCLKVEAAVLGAT 627  
Db 543 DEEPDWFEEKQVPPPHPPPLRYREPVLKFDGSLVLNDVMCKPGPESDPCCLKVEAAVLGAT 602  
QY 628 GPADSOHESQHGGLDQGEARPDALDGAALQPLLHTVTRAGSPDMPRDSIGYDSSVPSSE 687  
Db 603 GPADSOHESQHGGLDQGEARPDALDGAALQPLLHTVTRAGSPDMPRDSIGYDSSVPSSE 662  
QY 688 LSLPLMEGLSTDTQETSLTSSVSSGSGEPPALPSSKLLSSGCKADLCGRSYDEL 747  
Db 663 LSLPLMEGLSTDTQETSLTSSVSSGSGEPPALPSSKLLSSGCKADLCGRSYDEL 722  
QY 748 HAVAPL 753  
Db 723 HAVAPL 728  
RESULT 11  
US-09-874-503-18  
Sequence 18, Application US/09874503  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Hymowitz, Sarah G.  
APPLICANT: Tumas, Daniel  
APPLICANT: Starovasnik, Melissa A.  
APPLICANT: VanLookeren, Menno  
APPLICANT: Vandlen, Richard  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Yansura, Daniel  
FILE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381R1CIP3(US)  
CURRENT APPLICATION NUMBER: US/09/874,503  
CURRENT FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/253,646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: US 60/244,072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: US 60/242,837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/175,481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: US 60/191,007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/213,807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 60/172,096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: US 60/138,387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: US 60/134,287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US 60/131,022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: US 60/130,232  
PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: US 60/113,621  
 PRIOR FILING DATE: 1998-12-23  
 PRIOR APPLICATION NUMBER: US 60/085,579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: US 09/854,208  
 PRIOR FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: US 09/854,280  
 PRIOR FILING DATE: 2001-05-20  
 PRIOR APPLICATION NUMBER: US 09/816,744  
 PRIOR FILING DATE: 2001-03-22  
 PRIOR APPLICATION NUMBER: US 09/747,259  
 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: US 09/644,848  
 PRIOR FILING DATE: 2000-08-22  
 PRIOR APPLICATION NUMBER: US 09/380,142  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: US 09/380,138  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: US 09/311,832  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: US PCT/US01/06520  
 PRIOR FILING DATE: 2001-02-28  
 PRIOR APPLICATION NUMBER: US PCT/US00/34956  
 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: US PCT/US00/32678  
 PRIOR FILING DATE: 2000-12-01  
 PRIOR APPLICATION NUMBER: US PCT/US00/30873  
 PRIOR FILING DATE: 2000-11-10  
 PRIOR APPLICATION NUMBER: US PCT/US00/23328  
 PRIOR FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: US PCT/US00/15264  
 PRIOR FILING DATE: 2000-06-02  
 PRIOR APPLICATION NUMBER: US PCT/US00/07532  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: US PCT/US00/05841  
 PRIOR FILING DATE: 2000-03-02  
 PRIOR APPLICATION NUMBER: US PCT/US00/05601  
 PRIOR FILING DATE: 2000-03-01  
 PRIOR APPLICATION NUMBER: US PCT/US00/04341  
 PRIOR FILING DATE: 2000-02-18  
 PRIOR APPLICATION NUMBER: US PCT/US99/31274  
 PRIOR FILING DATE: 1999-12-30  
 PRIOR APPLICATION NUMBER: US PCT/US99/10733  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: US PCT/US99/05028  
 PRIOR FILING DATE: 1999-03-08  
 NUMBER OF SEQ ID NOS: 35  
 SEQ ID NO 18  
 LENGTH: 728  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-09-874-503-18

Query Match 92.3%; Score 3703; DB 22; Length 728;  
 Best Local Similarity 96.7%; Pred. No. 0;  
 Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;  
 QY 42 RKAAARPRICVANE-GVGPASRNSGLNITFYDNCITLNPVGVKHVIADAQNTISQY 100  
 DB 3 RASAGVPALFVSGEGVGPASRNSGLNITFYDNCITLNPVGVKHVIADAQNTISQY 62  
 QY 101 ACHDOAVATLSPALGIEFLKFRVILELSEGGCCQLLIDPKQLNNSPKFTGME 160  
 DB 63 ACHDOAVATLSPALGIEFLKFRVILELSEGGCCQLLIDPKQLNNSPKFTGME 122  
 QY 161 SQPLNNKFTDYFKVVPFFSINKESNYHFFFRTRACDQLLPDNLACKPFPKPRNLN 220  
 DB 123 SQPLNNKFTDYFKVVPFFSINKESNYHFFFRTRACDQLLPDNLACKPFPKPRNLN 182  
 QY 221 ISO-----HGSMDQVSDHAPNFCFRFFLYLHKHEGPFKRTCKQKQOTT 267  
 DB 183 ISQHGSDMQVSDHAPNFCFRFFLYLHKHEGPFKRTCKQKQOTT 242

QY 268 ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHVALKPVHSPNAGPIRAVAITVPLWISAF 327  
 DB 243 EMTSCLLQNVSPGDYIIELVDDTNTTRKVMHVALKPVHSPNAGPIRAVAITVPLWISAF 302  
 QY 328 ATLFTVMCRKKQOENITSHLDESSSTYTAALPRERLRPRPKVFLCYCKSKQOQNHMV 387  
 DB 303 ATLFTVMCRKKQOENITSHLDESSSTYTAALPRERLRPRPKVFLCYCKSKQOQNHMV 362  
 QY 388 VOCFAYFQDFCGCEVALDLMWDFSLCREGQRMWYIQIHESQFIIVVCSKGMKRYFYDKK 447  
 DB 363 VOCFAYFQDFCGCEVALDLMWDFSLCREGQRMWYIQIHESQFIIVVCSKGMKRYFYDKK 422  
 QY 448 NYKHKGGRGSGKGLFLVAVSAIAEKLRQAKQSSAALSAPFIIVFYDSCGDPGILD 507  
 DB 423 NYKHKGGRGSGKGLFLVAVSAIAEKLRQAKQSSAALSAPFIIVFYDSCGDPGILD 482  
 QY 508 LSTKTYELMDNLPCLCSHLHSDHGLQEPGQHTQGSRRNYFRSASGRSLYVAICNMHQFI 567  
 DB 483 LSTKTYELMDNLPCLCSHLHSDHGLQEPGQHTQGSRRNYFRSASGRSLYVAICNMHQFI 542  
 QY 568 DEEPWFKEQFYFPHPPPLRYREPVLKFDGSLVLDVNCCKPGPESDFCLKVEAAVLGAT 627  
 DB 543 DEEPWFKEQFYFPHPPPLRYREPVLKFDGSLVLDVNCCKPGPESDFCLKVEAAVLGAT 602  
 QY 628 GPADSOHESQHGGLDQDGEARPAALDGSAAALPILHTVKAQSPDMRDSGYDSSVPSSE 687  
 DB 603 GPADSOHESQHGGLDQDGEARPAALDGSAAALPILHTVKAQSPDMRDSGYDSSVPSSE 662  
 QY 688 LSLPLMEGLSTDOTETSLTESVSSSGGLGEEPPALPALKSLSSGCKADLCRSYTDL 747  
 DB 663 LSLPLMEGLSTDOTETSLTESVSSSGGLGEEPPALPALKSLSSGCKADLCRSYTDL 722  
 QY 748 HAVAPL 753  
 DB 723 HAVAPL 728

## RESULT 12

US-09-908-827-18  
 Sequence 18, Application US/09908827  
 GENERAL INFORMATION:  
 APPLICANT: Chen, Jian  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul  
 APPLICANT: Grimaldi, Christopher  
 APPLICANT: Gurney, Austin  
 APPLICANT: Li, Hanzhong  
 APPLICANT: Hillan, Kenneth  
 APPLICANT: Tumas, Daniel  
 APPLICANT: VanLookeren, Menno  
 APPLICANT: Vandlen, Richard  
 APPLICANT: Watanabe, Collin  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William  
 APPLICANT: Yansura, Daniel  
 TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
 FILE REFERENCE: P1381R1C1P1(US)  
 CURRENT APPLICATION NUMBER: US/09/908,827  
 CURRENT FILING DATE: 2001-07-18  
 PRIOR APPLICATION NUMBER: 60/085,579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/113,621  
 PRIOR FILING DATE: 1998-12-23  
 PRIOR APPLICATION NUMBER: 60/130,232  
 PRIOR FILING DATE: 1999-04-21  
 PRIOR APPLICATION NUMBER: 60/131,022  
 PRIOR FILING DATE: 1999-04-26  
 PRIOR APPLICATION NUMBER: 60/134,287  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: 60/138,387  
 PRIOR FILING DATE: 1999-06-09

PRIOR APPLICATION NUMBER: 60/172,096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/175,481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: 60/191,007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/213,807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 60/242,837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/244,072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: 09/311,832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/380,138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380,142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/644,848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 09/747,359  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/816,744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 09/854,208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/854,280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/US00/05601  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 18  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-908-827-18

Query Match 92.3%; Score 3703; DB 23; Length 728;  
Best Local Similarity 96.7%; Pred. No. 0;  
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;  
QY 42 RMKAAARPLCYANE-GYGPASRNSGLNTEKYDNTYLPVCKHVIADQNITISQY 100  
DB 3 RASASGVPALFVSGGQVGPASRNSGLNTEKYDNTYLPVCKHVIADQNITISQY 62  
QY 101 ACHQDQAVTILMSPGALGTEFLKGRVILBELKSEGRQCOQLIKDPKOLNSFKRTGME 160  
DB 63 ACHQDQAVTILMSPGALGTEFLKGRVILBELKSEGRQCOQLIKDPKOLNSFKRTGME 122

QY 161: SQPFLNKKFETDYFKVVPFPIKESNYHPFFTRACDILLQPDNLACKPFKPKRNLN 220  
DB 123: SQPFLNKKFETDYFKVVPFPIKESNYHPFFTRACDILLQPDNLACKPFKPKRNLN 182  
QY 221: ISO-----HGSDMQVSFDHAPNFCGFRFFLYLHYLKHGEPFKKTKCQSQTT 267  
DB 183: ISOHGSDMQVSFDHAPNFCGFRFFLYLHYLKHGEPFKKTKCQSQTT 242  
QY 268: ETTSCLLQNVSPGDYIELVDVDTNTRKVMHYALKPVHSPHAGPIRAVAITVPLVLSAF 327  
DB 243: EMTSCLLQNVSPGDYIELVDVDTNTRKVMHYALKPVHSPHAGPIRAVAITVPLVLSAF 302  
QY 328: ATLFTVNCRRKKOENIYSHLDEESSESTYTAALPRERLRPRKVFYLCYSSKQGNHNV 387  
DB 303: ATLFTVNCRRKKOENIYSHLDEESSESTYTAALPRERLRPRKVFYLCYSSKQGNHNV 362  
QY 388: VOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHESQFIIVVCSKGMKIFYDKK 447  
DB 363: VOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHESQFIIVVCSKGMKIFYDKK 422  
QY 448: NYKHGGGSGCKGELFLVAVSAIAEKLRQAKOSSAALSKEFIIVVCSKGMKIFYDKK 507  
DB 423: NYKHGGGSGCKGELFLVAVSAIAEKLRQAKOSSAALSKEFIIVVCSKGMKIFYDKK 482  
QY 508: LSTKYRLMDNLPQJCSHLHSRDHGLQEPGQRTQSGRRNYFRSKSGRSLYVAICNMHOFT 567  
DB 483: LSTKYRLMDNLPQJCSHLHSRDHGLQEPGQRTQSGRRNYFRSKSGRSLYVAICNMHOFT 542  
QY 568: DEEDPWFKEQFVPPHPPPLRYREPVLKESGLVNDVCKPGPESDCLKVEAAVLGAT 627  
DB 543: DEEDPWFKEQFVPPHPPPLRYREPVLKESGLVNDVCKPGPESDCLKVEAAVLGAT 602  
QY 628: GPADSQHESQHGGLDQDGEARPAALQDLSAALQPLHLYTVKAGSPSPDRSGIYDSSVPSSE 687  
DB 603: GPADSQHESQHGGLDQDGEARPAALQDLSAALQPLHLYTVKAGSPSPDRSGIYDSSVPSSE 662  
QY 688: LSLPLMEGLSTDQTTSTSLTESVSSSGIAGEEPALPSPKLLSSGCKADLCGRSYTDEL 747  
DB 663: LSLPLMEGLSTDQTTSTSLTESVSSSGIAGEEPALPSPKLLSSGCKADLCGRSYTDEL 722  
QY 748: HAVAPL 753  
DB 723: HAVAPL 728

## RESULT 13

US-09-908-827A-18  
Sequence 18, Application US/09908827A  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillan, Kenneth  
APPLICANT: Tumas, Daniel  
APPLICANT: VanLookeren, Menno  
APPLICANT: Vandlen, Richard  
APPLICANT: Watanabe, Collin  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William  
APPLICANT: Vansura, Daniel  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P138IPIC1(US)  
CURRENT APPLICATION NUMBER: US/09/908,827A  
CURRENT FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: 60/085,579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/113,621  
PRIOR FILING DATE: 1998-12-23



PRIOR APPLICATION NUMBER: 60/130,232  
 PRIOR FILING DATE: 1999-04-21  
 PRIOR APPLICATION NUMBER: 60/131,022  
 PRIOR FILING DATE: 1999-04-26  
 PRIOR APPLICATION NUMBER: 60/134,287  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: 60/138,387  
 PRIOR FILING DATE: 1999-06-09  
 PRIOR APPLICATION NUMBER: 60/172,096  
 PRIOR FILING DATE: 1999-12-23  
 PRIOR APPLICATION NUMBER: 60/175,481  
 PRIOR FILING DATE: 2000-01-11  
 PRIOR APPLICATION NUMBER: 60/191,007  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: 60/213,807  
 PRIOR FILING DATE: 2000-06-22  
 PRIOR APPLICATION NUMBER: 60/242,837  
 PRIOR FILING DATE: 2000-10-24  
 PRIOR APPLICATION NUMBER: 60/244,072  
 PRIOR FILING DATE: 2000-10-26  
 PRIOR APPLICATION NUMBER: 09/311,832  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: 09/380,138  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 09/380,142  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 09/644,848  
 PRIOR FILING DATE: 2000-08-22  
 PRIOR APPLICATION NUMBER: 09/747,259  
 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: 09/816,744  
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 PRIOR APPLICATION NUMBER: 09/854,208  
 PRIOR FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: 09/854,280  
 PRIOR FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: PCT/US99/05028  
 PRIOR FILING DATE: 1999-03-08  
 PRIOR APPLICATION NUMBER: PCT/US99/10733  
 PRIOR FILING DATE: 1999-05-14  
 PRIOR APPLICATION NUMBER: PCT/US99/31274  
 PRIOR FILING DATE: 1999-12-30  
 PRIOR APPLICATION NUMBER: PCT/US00/04341  
 PRIOR FILING DATE: 2000-02-18  
 PRIOR APPLICATION NUMBER: PCT/US00/05601  
 PRIOR FILING DATE: 2000-03-01  
 PRIOR APPLICATION NUMBER: PCT/US00/05841  
 PRIOR FILING DATE: 2000-03-02  
 PRIOR APPLICATION NUMBER: PCT/US00/07532  
 PRIOR FILING DATE: 2000-03-21  
 PRIOR APPLICATION NUMBER: PCT/US00/15264  
 PRIOR FILING DATE: 2000-06-02  
 PRIOR APPLICATION NUMBER: PCT/US00/23328  
 PRIOR FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: PCT/US00/30873  
 PRIOR FILING DATE: 2000-11-10  
 PRIOR APPLICATION NUMBER: PCT/US00/32678  
 PRIOR FILING DATE: 2000-12-01  
 PRIOR APPLICATION NUMBER: PCT/US00/34956  
 PRIOR FILING DATE: 2000-12-20  
 PRIOR APPLICATION NUMBER: PCT/US01/06520  
 PRIOR FILING DATE: 2001-02-28  
 NUMBER OF SEQ ID NOS: 39  
 SEQ ID NO 18  
 LENGTH: 728  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-09-908-827A-18

Query Match 92.3%; Score 3703; DB 23; Length 728;  
 Best Local Similarity 96.7%; Pred. No. 0;  
 Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RMAAARPRLCVANE-GVGPARNSGLNITFKYDNCITTLNPNVGRHVIADAQNTISQY 100  
 DB 3 RASASGVPAFLVSGGVGPARNSGLNITFKYDNCITTLNPNVGRHVIADAQNTISQY 62  
 QY 101 ACHDOAVATLSPALGIEFLKGRVILEELSEKQCCQQLILKDPKQLANSSFKRTGME 160  
 DB 63 ACHDOAVATLSPALGIEFLKGRVILEELSEKQCCQQLILKDPKQLANSSFKRTGME 122  
 QY 161 SQPLANKFETDYFKVVPFPIKSNESNYHPPFRACDILLQPDNLACPKFPKPNLN 220  
 DB 123 SQPLANKFETDYFKVVPFPIKSNESNYHPPFRACDILLQPDNLACPKFPKPNLN 182  
 QY 221 ISO-----HGSMDQVDFDAPHNFGFRFYLYLHKLHHEGPPKRTCKQBOIT 267  
 DB 183 ISOHSDMQVDFDAPHNFGFRFYLYLHKLHHEGPPKRTCKQBOIT 242  
 QY 268 ETTSCLLQNVSPGDYIIELVDOTNTTRVHYALKPVHSPWAGPRAVAITVPLVWISAF 327  
 DB 243 ETTSCLLQNVSPGDYIIELVDOTNTTRVHYALKPVHSPWAGPRAVAITVPLVWISAF 302  
 QY 328 ATLFTVMCRKQOENIYSHLDEESSESTYTAALPRERLRPRKPVFLCYSSKDGQGNHNV 387  
 DB 303 ATLFTVMCRKQOENIYSHLDEESSESTYTAALPRERLRPRKPVFLCYSSKDGQGNHNV 362  
 QY 388 VQCFATFLQDFCGCEVALDLHEDFSLCREGOREWVOKIHESQFIIVVCSKGMKFYVDKK 447  
 DB 363 VQCFATFLQDFCGCEVALDLHEDFSLCREGOREWVOKIHESQFIIVVCSKGMKFYVDKK 422  
 QY 448 NYKHGGGSGKGEFLFVAVSAIAEKLQAKOSSAAALSKEFIAYFYDSCGDPVPGILD 507  
 DB 423 NYKHGGGSGKGEFLFVAVSAIAEKLQAKOSSAAALSKEFIAYFYDSCGDPVPGILD 482  
 QY 508 LSTKYRLMDNLPLQCSHLSDHGLQEPGQTRGSGRRNYFRSKGSRSLYVAICNMHOFI 567  
 DB 483 LSTKYRLMDNLPLQCSHLSDHGLQEPGQTRGSGRRNYFRSKGSRSLYVAICNMHOFI 542  
 QY 568 DEEPDMFEKQFVFPHPPLRYREPVLEKFDGSLVNDVMCKPGPESDFCLKVEAAVLGAT 627  
 DB 543 DEEPDMFEKQFVFPHPPLRYREPVLEKFDGSLVNDVMCKPGPESDFCLKVEAAVLGAT 602  
 QY 628 GPADSQHSQHGGLDQDGEARLQDGAALQPLHVTYKAGSPSDMPROSGIYDSSVPSSE 687  
 DB 603 GPADSQHSQHGGLDQDGEARLQDGAALQPLHVTYKAGSPSDMPROSGIYDSSVPSSE 662  
 QY 688 LSLPLMEGLSTDTETSTSSLSYSSVSSGLGEEPPALPSKLLSSGCKADLCGRSYTDEL 747  
 DB 663 LSLPLMEGLSTDTETSTSSLSYSSVSSGLGEEPPALPSKLLSSGCKADLCGRSYTDEL 722  
 QY 748 HAVAPL 753  
 DB 723 HAVAPL 728

RESULT 14  
 US-10-000-157-18  
 ; Sequence 18, Application 05/10000157  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul L.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Li, Hanzhong  
 ; APPLICANT: Hymowitz, Sarah  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Starvasnik, Melissa  
 ; APPLICANT: VanLookeren, Menno  
 ; APPLICANT: Vandien, Richard  
 ; APPLICANT: Watanabe, Colin  
 ; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William  
APPLICANT: Yasura, Daniel  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381R1C1P4(US)  
CURRENT APPLICATION NUMBER: US/10/000,157  
CURRENT FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/130232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: 60/134287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/138387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/172096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/175481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: 60/191007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/213807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 60/242837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/244072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: 60/253646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 09/311832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/380138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/644848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 09/747259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/816744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 09/854208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/854280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/874503  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: 09/908827  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/929404  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 09/931836  
PRIOR FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
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PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
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PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
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PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/21066  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 18  
LENGTH: 728  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-000-157-18

Query Match 92.3%; Score 3703; DB 24; Length 728;  
Best Local Similarity 96.7%; Pred. No. 0;  
Matches 702; Conservative 8; Indels 14; Gaps 2;

QY 42 RKAAARPLCVANE-GVGPASRNSGLYNITFKYDNCTYLNPNVGVKVIADQNITISQY 100  
Db 3 RASAGVPALFVSGGVGASRNSGLYNITFKYDNCTYLNPNVGVKVIADQNITISQY 62  
QY 101 ACHDQAVTILWSPGALGIEFLAGFRVILEELKSEGCOCQOLILKDPKQNSFFKRTGME 160  
Db 63 ACHDQAVTILWSPGALGIEFLAGFRVILEELKSEGCOCQOLILKDPKQNSFFKRTGME 122  
QY 161 SDFELNMKFETDYFKVVPFSPKSNESVHPFFETTRACDILLQPDNLACKPFWKPRNLN 220  
Db 123 SDFELNMKFETDYFKVVPFSPKSNESVHPFFETTRACDILLQPDNLACKPFWKPRNLN 182  
QY 221 ISQ-----HGSDQVVSFDHAPNFGFRFFYLHYLKLHKGPFKRTCKEQTT 267  
Db 183 ISQHGSDQVVSFDHAPNFGFRFFYLHYLKLHKGPFKRTCKEQTT 242  
QY 268 ETTSCLLQNVSPGDYIIELVDDTNTTKVMHYALAPVHSPWAGPIRAVATVPLVVISAF 327  
Db 243 ETTSCLLQNVSPGDYIIELVDDTNTTKVMHYALAPVHSPWAGPIRAVATVPLVVISAF 302  
QY 328 ATLFTVMCRKQENIYSHLDESSSTYTAALPRERLRPRPKVFLCYSSKDGQNHMY 387  
Db 303 ATLFTVMCRKQENIYSHLDESSSTYTAALPRERLRPRPKVFLCYSSKDGQNHMY 362  
QY 388 VOCFAFLQDFCGCEVALDIEDFSLCRGQREWIQIHESQFIIVVCSKGMKYPVDKK 447  
Db 363 VOCFAFLQDFCGCEVALDIEDFSLCRGQREWIQIHESQFIIVVCSKGMKYPVDKK 422  
QY 448 NYKKGGGSGKGELFLVAVSAIAEKLQAKOSSAALSFIAYFYDYCEGDVPGILD 507  
Db 423 NYKKGGGSGKGELFLVAVSAIAEKLQAKOSSAALSFIAYFYDYCEGDVPGILD 482  
QY 508 LSTKYRLMDNLPOLCSHLHSDHGLQPGHTRGSRNRYFRSKSGSLVAICNHHQFI 567  
Db 483 LSTKYRLMDNLPOLCSHLHSDHGLQPGHTRGSRNRYFRSKSGSLVAICNHHQFI 542  
QY 568 DEEDPWFKEQVPPHPPPLRYREPVLKEFDGSLVLDNVCKPGPESDFCLKVEAAVLGAT 627  
Db 543 DEEDPWFKEQVPPHPPPLRYREPVLKEFDGSLVLDNVCKPGPESDFCLKVEAAVLGAT 602  
QY 628 GPADSOHESOHGGLDQGEARPAIDCSAALQPLLAHTVKGSPSDMPDSCGYDSSVPSSE 687  
Db 603 GPADSOHESOHGGLDQGEARPAIDCSAALQPLLAHTVKGSPSDMPDSCGYDSSVPSSE 662

QY 688 LSLPLMGLSTQDTSTSSLSVSSSGLEPPALPSKLLSSGSKADLGRSYDEL 747  
DB 663 LSLPLMGLSTQDTSTSSLSVSSSGLEPPALPSKLLSSGSKADLGRSYDEL 722  
QY 748 HAVAPL 753  
DB 723 HAVAPL 728

## RESULT 15

US-09-912-157-12

Sequence 12, Application US/0912157

GENERAL INFORMATION:

APPLICANT: Presnell, Scott R.

APPLICANT: Kuestner, Rolf E.

APPLICANT: Gao, Zeren

TITLE OF INVENTION: Human Cytokine Receptor

FILE REFERENCE: 00-49

CURRENT APPLICATION NUMBER: US/09/912.157

CURRENT FILING DATE: 2001-07-23

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 739

TYPE: PRT

ORGANISM: Mouse

US-09-912-157-12

Query Match 84.4%; Score 3387; DB 23; Length 739;  
Best Local Similarity 85.2%; Pred. No. 0;  
Matches 645; Conservative 37; Mismatches 53; Indels 22; Gaps 6;

QY 1 MAPLQICSVFTVNACLNGSLAVAGGSGRARGADTCGRMAKAAARPLRCVANEVGP 60  
DB 1 MAPLQICSVFTVNACLNGSLAVAGGSGRARGADTCGRMAKAAARPLRCVANEVGP 46  
QY 61 ASRNSGLNITFYDNCCTYLP-VGRHVADAGNITISQACHQVAVTILMSPGALGI 119  
DB 47 ASRNSGLNITFYDNCCTYLPNGGGKHAIDAGNITISQACHQVAVTILMSPGALGI 106  
QY 120 EFLKGFVILEELKSGRCCQQLILKDPKQLNSFKRTGHSQPLNKKFTDYFVKVP 179  
DB 107 EFLKGFVILEELKSGRCCQQLILKDPKQLNSFKRTGHSQPLNKKFTDYFVKVP 166  
QY 180 FPSIKNESNTHPEFFTRACDILLQDNLACKPFWKPRNINISQGSNDQVSDHAPHNF 239  
DB 167 FPSIKNESNTHPEFFTRACDILLQDNLACKPFWKPRNINISQGSNDQVSDHAPHNF 226  
QY 240 GFRFPYLYKHEGPFRTCKOBOTTTSCLLQNVSPGYIIELVDDTNTTKVMHY 299  
DB 227 GFRGFVLYKHEGPFRTCKOBOTTTSCLLQNVSPGYIIELVDDTNTTKVMHY 286  
QY 300 ALKPVHSPWAGPTRAIVATVPLVVISAPATLFTVMCKKQENITSHLDESSSSTYTA 359  
DB 287 VYKSVOSPWAGPTRAIVATVPLVVISAPATLFTVMCKKQENITSHLDESSSSTYTA 346  
QY 360 ALPRERLRPKVFLCYSSKQGNMNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGOR 419  
DB 347 ALPRERLRPKVFLCYSSKQGNMNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGOR 406  
QY 420 EWLKTHESQPIIVVCSKGMKYFYDKKNTKKGSGGSGKGELEFLVAVSAIAEKLROAK 479  
DB 407 EWLKTHESQPIIVVCSKGMKYFYDKKNTKKGSGGSGKGELEFLVAVSAIAEKLROAK 466  
QY 480 QSSAALSKPIAVFYDSCGDPGILDLSTKYRLMDNLPQLCSHLHSDHGLQEP-CQH 538  
DB 467 QSSAALSKPIAVFYDSCGDPGILDLSTKYRLMDNLPQLCSHLHSDHGLQEP-CQH 523  
QY 539 TROGSRNYPKSGSLYVACNMHOPIDEEDPWEKQFVPPHPPPLRYEPVLEKFD 598  
DB 524 TROGSRNYPKSGSLYVACNMHOPIDEEDPWEKQFVPPHPPPLRYEPVLEKFD 583

QY 599 GLVLDVNMCKPESDPCFLKVEAAVLGATGPADSQH--ESQHGGLDODGEARPALDGSAA 656  
DB 584 GLVLDVNMCKPESDPCFLKVEAAVLGATGPADSQH--ESQHGGLDODGEARPALDGSAA 643  
QY 657 LQPLLTHTVKAQSPDMPRDSGIYDSSVPSSELSLPLMGLSTQDTSTSSLSVSSSGI 716  
DB 644 LQPLLTHTVKAQSPDMPRDSGIYDSSVPSSELSLPLMGLSTQDTSTSSLSVSSSGI 703  
QY 717 GEEPPALPSKLLSSGSKADLGRSYTDELHAPL 753  
DB 704 GEEPPALPSKLLSSGSKADLGRSYTDELHAPL 739

Search completed: May 16, 2003, 13:48:57  
Job time: 158 secs